

20					25					30					
Leu	Thr	Leu	Ser	Val	Thr	Leu	Leu	Gly	Gly	Val	Thr	Ile	Leu	Ser	Ile
		35					40					45			
Ile	Gly	Ala	Pro	Leu	Leu	Thr	Arg	Met	Met	Leu	Ser	Ser	Glu	Gly	Gln
	50					55					60				
Val	Asn	Val	Val	Met	Ser	Thr	Ala	Phe	Ala	Tyr	Trp	Leu	Leu	Pro	Gln
	65					70					75				80
Ile	Phe	Phe	Tyr	Gly	Leu	Phe	Ala	Leu	Phe	Met	Ala	Val	Leu	Asn	Thr
				85					90					95	
Arg	Glu	Val	Phe	Lys	Pro	Gly	Ala	Trp	Ala	Pro	Val	Val	Asn	Asn	Val
			100					105					110		
Ile	Thr	Leu	Thr	Val	Leu	Gly	Val	Tyr	Met	Val	Leu	Pro	Ala	Arg	Leu
	115					120					125				
His	Pro	His	Glu	Gln	Val	Gly	Ile	Phe	Asp	Pro	Gln	Ile	Ile	Phe	Leu
	130					135					140				
Gly	Val	Gly	Thr	Thr	Leu	Gly	Val	Val	Ala	Gln	Cys	Leu	Ile	Met	Ile
	145					150					155				160
Pro	Tyr	Leu	Arg	Arg	Ala	Gly	Ile	Asp	Met	Arg	Pro	Leu	Trp	Gly	Ile
				165				170						175	
Asp	Ala	Arg	Leu	Lys	Gln	Phe	Gly	Gly	Met	Ala	Met	Ala	Ile	Ile	Val
			180					185					190		
Tyr	Val	Ala	Ile	Ser	Gln	Phe	Gly	Tyr	Ile	Ile	Thr	Thr	Arg	Ile	Ala
	195					200					205				
Ser	Ile	Ala	Asp	Asp	Ala	Ala	Pro	Phe	Ile	Tyr	Gln	Gln	His	Trp	Met
	210					215					220				
Leu	Leu	Gln	Val	Pro	Tyr	Gly	Ile	Ile	Gly	Val	Thr	Leu	Leu	Thr	Ala
	225					230					235				240
Ile	Met	Pro	Arg	Leu	Ser	Arg	Asn	Ala	Ala	Asp	Gly	Asp	Asp	Arg	Ala
				245				250						255	

Val	Val	Ser	Asp	Leu	Gln	Leu	Gly	Ser	Lys	Leu	Thr	Phe	Ile	Ala	Leu
			260					265					270		
Ile	Pro	Ile	Val	Val	Phe	Phe	Thr	Ala	Phe	Gly	Val	Pro	Ile	Ala	Asn
		275					280					285			
Gly	Leu	Phe	Ala	Tyr	Gly	Gln	Phe	Asp	Ala	Asn	Ala	Ala	Asn	Ile	Leu
	290					295					300				
Gly	Trp	Thr	Leu	Ser	Phe	Ser	Ala	Phe	Thr	Leu	Ile	Pro	Tyr	Ala	Leu
	305					310					315			320	
Val	Leu	Leu	His	Leu	Arg	Val	Phe	Tyr	Ala	Arg	Glu	Glu	Val	Trp	Thr
			325						330				335		
Pro	Thr	Phe	Ile	Ile	Ala	Gly	Ile	Thr	Ala	Thr	Lys	Val	Val	Leu	Ser
			340					345					350		

Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu
 355 360 365
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly
 370 375 380
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu
 385 390 395 400
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala
 405 410 415
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe
 420 425 430
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val
 435 440 445
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser
 450 455 460
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro
 465 470 475 480
 Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val
 485 490 495
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser
 500 505 510
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val
 515 520 525
 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe
 530 535 540
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln
 545 550 555 560
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp
 565 570 575
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala
 580 585 590
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu
 595 600 605
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn
 610 615 620
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala
 625 630 635 640
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala
 645 650 655
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala
 660 665 670

Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala
 675 680 685
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp
 690 695 700
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu
 705 710 715 720
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala
 725 730 735
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr
 740 745 750
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu
 755 760 765
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr
 770 775 780
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val
 785 790 795 800
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser
 805 810 815
 Ser Thr Asn Glu Gln Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser
 820 825 830
 Ala Thr Pro Glu Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln
 835 840 845
 Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr
 850 855 860
 Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu
 865 870 875 880
 Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr
 885 890 895
~~Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr~~
~~900 905 910~~
 Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile
 915 920 925
 Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp
 930 935 940
 Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp
 945 950 955 960
 Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile
 965 970 975
 Ala Glu Val Gln Leu Val Gly Trp
 980

```
<210> 595
<211> 915
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(892)  
<223> RXA01807
```

<400> 595																	60
gctcaccgag ctggacacca agctccgcgc agtgcaggaa gaacacggcg agctggaaat																	
gcagtggtcg gaactcggcg aggaaatcga gggctagttc atg ccg tcg gca ggc																	115
Met Pro Ser Ala Gly																	
1 5																	
gag gag att tta gag cag cgc gca cag ctg gag ttt gat cag cgc cgc																	163
Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg																	
10 15 20																	
gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggg																	211
Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly																	
25 30 35																	
ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc																	259
Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val																	
40 45 50																	
gct gtc ccc acc gtg gtg tta agt tcc atg ccg cgt tat gca agt tct																	307
Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser																	
55 60 65																	
cac cgc cag ccg atg tcg gac caa tgg ctc gcc gac gcg ctg caa gac																	355
His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp																	
70 75 80 85																	
ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc																	403
Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly																	
90 95 100																	
tat ttt acc tcc gct tct cag gtg cgt gtg gtc gct gcg tgg ctg cag																	451
Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln																	
105 110 115																	
aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc																	499
Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile																	
120 125 130																	
atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc																	547
Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr																	
135 140 145																	
gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat																	595
Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn																	
150 155 160 165																	
gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg																	643
Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu																	
170 175 180																	

ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act 691
 Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr
 185 190 195

gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa 739
 Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu
 200 205 210

atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc 787
 Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val
 215 220 225

tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc 835
 Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile
 230 235 240 245

gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc 883
 Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr
 250 255 260

aaa gcg ctt taggtttcgt ccgtctctga cag 915
 Lys Ala Leu

<210> 596
 <211> 264
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 596
 Met Pro Ser Ala Gly Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu
 1 5 10 15

Phe Asp Gln Arg Arg Ala Asp Val Val Met Ile Gly Ser Gln Val Val
 20 25 30

Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu
 35 40 45

Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro
 50 55 60

Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala
 65 70 75 80

Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser
 85 90 95

Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val
 100 105 110

Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile
 115 120 125

Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala
 130 135 140

Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr
 145 150 155 160

Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly
 165 170 175

Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr
 180 185 190

Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg
 195 200 205

Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys
 210 215 220

Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys
 225 230 235 240

Asp Phe Ser Leu Ile Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys
 245 250 255

Ala Gly Leu Gln Thr Lys Ala Leu
 260

<210> 597
 <211> 1461
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1438)
 <223> RXN02754

<400> 597
 attatgaagc catcgaggtt ggtgtggcct acaaggggtga tcatgctgtg atagtgggtg 60

agttcactgt agctcccgct gattccgtag aatcaacaga gtg aat acc aat ccg 115
 Val Asn Thr Asn Pro
 1 5

tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163
 Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr
 10 15 20

gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211
 Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg
 25 30 35

ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga 259
 Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg
 40 45 50

tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac 307
 Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp
 55 60 65

ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac 355
 Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp
 70 75 80 85

cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403
 Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp

	90	95	100	
ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act				451
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr	105	110	115	
gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg				499
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu	120	125	130	
tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg				547
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met	135	140	145	
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc				595
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg	150	155	160	165
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct				643
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala	170	175	180	
gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att				691
Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile	185	190	195	
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac				739
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn	200	205	210	
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa				787
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu	215	220	225	
tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc				835
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr	230	235	240	245
caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca gac ctt ggt ggc				883
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro Asp Leu Gly Gly	250	255	260	
gta cgt atc gac tcc ggc gaa cta ggt gtc ctt gcc cga aag gtc cgc				931
Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg	265	270	275	
aag cag ctc gac gat ctc aac gcc cac aac acc aag att gtg gtc tcc				979
Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser	280	285	290	
tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt				1027
Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val	295	300	305	
gac gtc ttt ggc gtt ggc acc tcc gtt gtc aca ggt tct ggc gca cca				1075
Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro	310	315	320	325

acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg
1123

Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val
330 335 340

gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct
1171

Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala
345 350 355

gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac
1219

Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr
360 365 370

cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc
1267

Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser
375 380 385

ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct
1315

Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro
390 395 400 405

act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta
1363

Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu
410 415 420

cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act
1411

Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr
425 430 435

cgt ttc gtg ggt ttc ccg ccg gcc gct tagacaattc ggtctcacca
1458

Arg Phe Val Gly Phe Pro Pro Ala Ala
440 445

aac
1461

<210> 598

<211> 446

<212> PRT

<213> Corynebacterium glutamicum

<400> 598

Val Asn Thr Asn Pro Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu
1 5 10 15

Leu Thr Asp Lys Tyr Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp
20 25 30

Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
35 40 45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
50 55 60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
 65 70 75 80
 Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
 85 90 95
 Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
 100 105 110
 Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu
 115 120 125
 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser
 130 135 140
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu
 145 150 155 160
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg
 165 170 175
 Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala
 180 185 190
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr
 195 200 205
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe
 210 215 220
 Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp
 225 230 235 240
 Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly
 245 250 255
 Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu
 260 265 270
 Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr
 275 280 285
 Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu
 290 295 300
 Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr Ser Val Val Thr
 305 310 315 320
 Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val
 325 330 335
 Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly
 340 345 350
 Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile
 355 360 365
 Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys
 370 375 380

Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile
 385 390 395 400

Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys
 405 410 415

Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu
 420 425 430

Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro Ala Ala
 435 440 445

<210> 599

<211> 871

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(871)

<223> FRXA02405

<400> 599

attatgaagc catcgaggtt ggtgtggcct acaagggtga tcatgcgtgg atagtgggtgg 60

agttcactgt agtccccgct gattccgtag aatcaacaga gtg aat acc aat ccg 115
 Val Asn Thr Asn Pro
 1 5

tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163
 Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr
 10 15 20

gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211
 Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg
 25 30 35

ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga 259
 Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg
 40 45 50

tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac 307
 Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp
 55 60 65

ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac 355
 Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp
 70 75 80 85

cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403
 Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp
 90 95 100

ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act 451
 Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr
 105 110 115

gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg 499
 Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu
 120 125 130

tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg 547
 Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met
 135 140 145

gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc 595
 Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg
 150 155 160 165

acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct 643
 Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala
 170 175 180

gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att 691
 Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile
 185 190 195

cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac 739
 Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn
 200 205 210

gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa 787
 Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu
 215 220 225

tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc 835
 Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr
 230 235 240 245

caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca 871
 Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro
 250 255

<210> 600

<211> 257

<212> PRT

<213> Corynebacterium glutamicum

<400> 600

Val Asn Thr Asn Pro Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu
 1 5 10 15

Leu Thr Asp Lys Tyr Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp
 20 25 30

Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
 35 40 45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
 50 55 60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
 65 70 75 80

Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
 85 90 95

Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
 100 105 110

Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu
115 120 125

Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser
130 135 140

Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu
145 150 155 160

Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg
165 170 175

Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala
180 185 190

Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr
195 200 205

Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe
210 215 220

Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp
225 230 235 240

Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly
245 250 255

Pro

<210> 601

<211> 509

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(486)

<223> FRXA02754

<400> 601

ccc aca aac acc aag att gtg gtc tcc tcc gac ctg gat gaa ttc gcc 48
Pro Thr Asn Thr Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala
1 5 10 15

atc gcg ggt ctt cgc ggc gaa cca gtt gac gtc ttt ggc gtt ggc acc 96
Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr
20 25 30

tcc gtt gtc aca ggt tct ggc gca cca acc gct ggc ctc gtg tac aag 144
Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys
35 40 45

atc ggg gaa gtt gcc ggt cac cct gtg gcc aag cgt tcc cga aac aag 192
Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys
50 55 60

gaa agc tac ggt ggt ggc aag aag gct gtg cgc acc cac cgc aag tcc 240
Glu Ser Tyr Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser
65 70 75 80

ggt acc gca atc gaa gaa atc gtc tac cca ttc aat gcc gaa gca cca 288
 Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro
 85 90 95

gat act gga aag ctc gac act ttg agc ctg acc atc cca ttg atg cgc 336
 Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg
 100 105 110

gac ggt gaa atc gtt cca ggt ttg cct act ttg gaa gat tcc cga gcg 384
 Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala
 115 120 125

tat ttg gcc aag caa ttg gtc tct tta cca tgg gaa ggc ctt gca ctg 432
 Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu
 130 135 140

tct cgc gat gag cct gtt ttg cac act cgt ttc gtg ggt ttc ccg ccg 480
 Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro
 145 150 155 160

gcc gct tagacaattc ggtctcacca aac 509
 Ala Ala

<210> 602

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 602

Pro Thr Asn Thr Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala
 1 5 10 15

Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr
 20 25 30

Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys
 35 40 45

Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys
 50 55 60

Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser
 65 70 75 80

Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro
 85 90 95

Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg
 100 105 110

Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala
 115 120 125

Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu
 130 135 140

Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro
 145 150 155 160

Ala Ala

<210> 603

<211> 960

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(937)

<223> RXA02112

<400> 603

```

tgaatccgtg gcggcaccgg cgcgagtcgc tttggaaagg atgctatctg ttgttccagc 60
agctcctggt actcctagct cctcgaagga tgcgtaattt atg act acc cat att 115
                                     Met Thr Thr His Ile
                                     1                               5

gac cgc atc gtt ggc gca gcg tta tcc gag gat gcg cca tgg ggc gac 163
Asp Arg Ile Val Gly Ala Ala Leu Ser Glu Asp Ala Pro Trp Gly Asp
                               10                               15                               20

att acc tcc gac act ttt atc cca gga tcg gcg cag ctg agc gcc aag 211
Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala Gln Leu Ser Ala Lys
                               25                               30                               35

gtt gtt gcc cgg gag cca ggt gtg ttc agc ggg cag gcg ctt tta gac 259
Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly Gln Ala Leu Leu Asp
                               40                               45                               50

gcc tcc ttc cgg ctc gtc gat cct agg ata aac gca tcc ctt aag gtg 307
Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn Ala Ser Leu Lys Val
                               55                               60                               65

gct gat ggt gac agc ttt gaa acc ggg gac atc cta gga aca att acc 355
Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile Leu Gly Thr Ile Thr
                               70                               75                               80                               85

ggc agt gct aga agc atc ctc cgt tca gag cgc att gct ctc aac ttc 403
Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg Ile Ala Leu Asn Phe
                               90                               95                               100

att cag agg acg tcc ggc atc gct aca ttg aca tcg tgc tat gtt gca 451
Ile Gln Arg Thr Ser Gly Ile Ala Thr Leu Thr Ser Cys Tyr Val Ala
                               105                               110                               115

gag gtt aaa ggc acc aaa qcc cgc att gtt gat acc cgg aaa acc aca 499
Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp Thr Arg Lys Thr Thr
                               120                               125                               130

ccc ggc ctg cgc atc att gaa cgc caa gct gtc cgt gac ggt ggc gga 547
Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val Arg Asp Gly Gly Gly
                               135                               140                               145

ttt aat cac cga gcc acc ttg tcc gat gct gtc atg gtg aaa gat aac 595
Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val Met Val Lys Asp Asn
                               150                               155                               160                               165

```

cat ctc gca gcc atc gca tcc cag ggg ctc agc atc act gaa gcg ctg 643
 His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser Ile Thr Glu Ala Leu
 170 175 180

tcg aat atg aaa gct aaa ctc ccc cac acc acc cat gtg gaa gtc gaa 691
 Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr His Val Glu Val Glu
 185 190 195

gtt gat cat ata gag cag atc gaa cca gtt ctt gct gct ggt gtg gac 739
 Val Asp His Ile Glu Gln Ile Glu Pro Val Leu Ala Ala Gly Val Asp
 200 205 210

acc atc atg ttg gat aat ttc acc att gat cag ctc atc gaa ggc gtt 787
 Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln Leu Ile Glu Gly Val
 215 220 225

gat ctc att ggt gga cgt gca ctg gtg gaa gca tct ggc gga gtc aac 835
 Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala Ser Gly Gly Val Asn
 230 235 240 245

ctc aac acc gcg gga aag att gca tca acc ggt gtc gac gtc att tcc 883
 Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly Val Asp Val Ile Ser
 250 255 260

gtt gga gcg ctt acc cat tct gtg cat gca ctt gac cta gga ctc gat 931
 Val Gly Ala Leu Thr His Ser Val His Ala Leu Asp Leu Gly Leu Asp
 265 270 275

att ttc taatgctcta ccttgataat gca 960
 Ile Phe

<210> 604
 <211> 279
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 604
 Met Thr Thr His Ile Asp Arg Ile Val Gly Ala Ala Leu Ser Glu Asp
 1 5 10 15

Ala Pro Trp Gly Asp Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala
 20 25 30

Gln Leu Ser Ala Lys Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly
 35 40 45

Gln Ala Leu Leu Asp Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn
 50 55 60

Ala Ser Leu Lys Val Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile
 65 70 75 80

Leu Gly Thr Ile Thr Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg
 85 90 95

Ile Ala Leu Asn Phe Ile Gln Arg Thr Ser Gly Ile Ala Thr Leu Thr
 100 105 110

Ser Cys Tyr Val Ala Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp
 115 120 125

Thr Arg Lys Thr Thr Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val
 130 135 140

Arg Asp Gly Gly Gly Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val
 145 150 155 160

Met Val Lys Asp Asn His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser
 165 170 175

Ile Thr Glu Ala Leu Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr
 180 185 190

His Val Glu Val Glu Val Asp His Ile Glu Gln Ile Glu Pro Val Leu
 195 200 205

Ala Ala Gly Val Asp Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln
 210 215 220

Leu Ile Glu Gly Val Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala
 225 230 235 240

Ser Gly Gly Val Asn Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly
 245 250 255

Val Asp Val Ile Ser Val Gly Ala Leu Thr His Ser Val His Ala Leu
 260 265 270

Asp Leu Gly Leu Asp Ile Phe
 275

<210> 605
 <211> 1407
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1384)
 <223> RXA02111

<400> 605
 gcttgcgggga acaccgcacc gccaccccaa actgttcaga ttccaaagat aaattctgac 60

gctcattcca gccaccggtt tagaagaaaa gaccccaatc atg acc acc tca atc 115
 Met Thr Thr Ser Ile
 1 5

acc cca tct gtc aac ctt gca ttg aaa aat gcc aat agc tgc aac agt 163
 Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala Asn Ser Cys Asn Ser
 10 15 20

gaa ctc aaa gac gga ccc tgg ttc ctc gac cag ccc gga atg ccg gat 211
 Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln Pro Gly Met Pro Asp
 25 30 35

gtc tac ggc ccc ggc gcg tca caa aac gat ccg atc cct gcg cat gct 259
 Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro Ile Pro Ala His Ala

40	45	50	
ccg cgc cag cag gtt ctc ccc gag gag tac cag cgc gca agt gat gac			307
Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln Arg Ala Ser Asp Asp			
55	60	65	
gaa ctg cat cgt agg atc cgg gaa gcg aaa gac acc ctg ggt gac aaa			355
Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp Thr Leu Gly Asp Lys			
70	75	80	85
gtg gtt atc cta gga cac ttc tac cag cgc gat gaa gtt atc caa cac			403
Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp Glu Val Ile Gln His			
90	95	100	
gca gat ttt gtt ggt gac tct ttc caa ctt gcc cgc gct gcc aaa acc			451
Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala Arg Ala Ala Lys Thr			
105	110	115	
cga ccc gag gcg gaa gcg att gtg ttc tgc ggt gtg cac ttc atg gct			499
Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly Val His Phe Met Ala			
120	125	130	
gaa acc gct gat ctg tta tcc acg gat gaa caa tca gtg atc ctc ccc			547
Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln Ser Val Ile Leu Pro			
135	140	145	
aac ctt gcc gca ggt tgc tcc atg gca gac atg gct gac ctt gat tcc			595
Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met Ala Asp Leu Asp Ser			
150	155	160	165
gtc gaa gac tgc tgg gag caa ctc acc tca att tat ggc gat gac acc			643
Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile Tyr Gly Asp Asp Thr			
170	175	180	
ctg atc cct gtg acc tac atg aat tcc tct gca gcg ctc aaa ggt ttc			691
Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala Ala Leu Lys Gly Phe			
185	190	195	
gtg ggt gag cac ggc gga att gta tgc acc tcc tca aat gca cgt tcc			739
Val Gly Glu His Gly Gly Ile Val Cys Thr Ser Ser Asn Ala Arg Ser			
200	205	210	
gta tgg gag tgg gag ttt gaa gga ggc caa tga gtc ctg ttc ttc ccc			787
Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg Val Leu Phe Phe Pro			
215	220	225	
gat cag cac ttg ggt cga aac acc gcg aaa gcc atg ggc att ggg atc			835
Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala Met Gly Ile Gly Ile			
230	235	240	245
gat caa atg ccc ctg tgg aat ccc aac aaa cca ctg ggt ggc aac acc			883
Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro Leu Gly Gly Asn Thr			
250	255	260	
gtt tcc gag cta gaa aac gca aag gta ctg ctc tgg cat ggt ttc tgc			931
Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu Trp His Gly Phe Cys			
265	270	275	
tct gta cac aag cgc ttt act gtc gag cag atc aac aaa gcc cgc gcc			979
Ser Val His Lys Arg Phe Thr Val Glu Gln Ile Asn Lys Ala Arg Ala			
280	285	290	

gag tac ccc gac gtt cac gtc atc gtg cac cct gaa tcc ccc atg cca
1027

Glu Tyr Pro Asp Val His Val Ile Val His Pro Glu Ser Pro Met Pro
295 300 305

gtt gtt gac gcc gcc gac tca tcc gga tcc act gac ttc att gtg aaa
1075

Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr Asp Phe Ile Val Lys
310 315 320 325

gcc att caa gca gca ccg gca gga tct acc ttt gcg atc ggc acc gaa
1123

Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe Ala Ile Gly Thr Glu
330 335 340

atc aac ttg gtt cag cgc ctg gca gcc cag tac ccg cag cac acc atc
1171

Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr Pro Gln His Thr Ile
345 350 355

ttc tgc ctc gac cct gtc atc tgc cca tgc tcc acc atg tat cgc att
1219

Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser Thr Met Tyr Arg Ile
360 365 370

cac cct ggt tac ctg gcc tgg gca ctt gag gag ttg gtg gct gga aac
1267

His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu Leu Val Ala Gly Asn
375 380 385

gtg att aac cag att tct gtc tct gaa tcc gtg gcg gca ccg gcg cga
1315

Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val Ala Ala Pro Ala Arg
390 395 400 405

gtc gct ttg gaa agg atg cta tct gtt gtt cca gca gct cct gtt act
1363

Val Ala Leu Glu Arg Met Leu Ser Val Val Pro Ala Ala Pro Val Thr
410 415 420

cct agc tcc tcg aag gat gcg taatttatga ctacccatat tga
1407

Pro Ser Ser Ser Lys Asp Ala
425

<210> 606

<211> 428

<212> PRT

<213> Corynebacterium glutamicum

<400> 606

Met Thr Thr Ser Ile Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala
1 5 10 15

Asn Ser Cys Asn Ser Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln
20 25 30

Pro Gly Met Pro Asp Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro
35 40 45

Ile Pro Ala His Ala Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln
 50 55 60
 Arg Ala Ser Asp Asp Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp
 65 70 75 80
 Thr Leu Gly Asp Lys Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp
 85 90 95
 Glu Val Ile Gln His Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala
 100 105 110
 Arg Ala Ala Lys Thr Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly
 115 120 125
 Val His Phe Met Ala Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln
 130 135 140
 Ser Val Ile Leu Pro Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met
 145 150 155 160
 Ala Asp Leu Asp Ser Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile
 165 170 175
 Tyr Gly Asp Asp Thr Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala
 180 185 190
 Ala Leu Lys Gly Phe Val Gly Glu His Gly Gly Ile Val Cys Thr Ser
 195 200 205
 Ser Asn Ala Arg Ser Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg
 210 215 220
 Val Leu Phe Phe Pro Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala
 225 230 235 240
 Met Gly Ile Gly Ile Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro
 245 250 255
 Leu Gly Gly Asn Thr Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu
 260 265 270
 Trp His Gly Phe Cys Ser Val His Lys Arg Phe Thr Val Glu Gln Ile
 275 280 285
 Asn Lys Ala Arg Ala Glu Tyr Pro Asp Val His Val Ile Val His Pro
 290 295 300
 Glu Ser Pro Met Pro Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr
 305 310 315 320
 Asp Phe Ile Val Lys Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe
 325 330 335
 Ala Ile Gly Thr Glu Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr
 340 345 350
 Pro Gln His Thr Ile Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser
 355 360 365

Thr Met Tyr Arg Ile His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu
370 375 380

Leu Val Ala Gly Asn Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val
385 390 395 400

Ala Ala Pro Ala Arg Val Ala Leu Glu Arg Met Leu Ser Val Val Pro
405 410 415

Ala Ala Pro Val Thr Pro Ser Ser Ser Lys Asp Ala
420 425

<210> 607

<211> 954

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(931)

<223> RXA01073

<400> 607

taaccgactc cagcactaaa ctccaaaccc ttggcccgcga ccgccaaagt ttagcgcgcc 60

ccaagacacc accgcgccat gtttgcctag gattaggtac atg aca aac act caa 115
Met Thr Asn Thr Gln
1 5

acc gag atc att aat gaa cta aag gtg agc cca gca atc gac gtg gcc 163
Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro Ala Ile Asp Val Ala
10 15 20

aag gaa gtt gaa ttc cgt gtg cag ttc ctc gtc gat tac ctg cgg gct 211
Lys Glu Val Glu Phe Arg Val Gln Phe Leu Val Asp Tyr Leu Arg Ala
25 30 35

tcc cat aca aaa ggc ttt gtt ctt ggt att tca ggt ggc cag gat tcc 259
Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser Gly Gly Gln Asp Ser
40 45 50

act ctt gcg gga cga ctc acg cag ctg gca gta gag cgc att cgt gcg 307
Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val Glu Arg Ile Arg Ala
55 60 65

gaa gaa aac agc acg gat tat gtc ttc tac gca gtt cgc ctc ccc tac 355
Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala Val Arg Leu Pro Tyr
70 75 80 85

gcg atc caq qca gat gag gac gat gcg caa gtt gca ttg gaa ttc atc 403
Ala Ile Gln Ala Asp Glu Asp Asp Ala Gln Val Ala Leu Glu Phe Ile
90 95 100

gca cct gac aag agc gtg acc gtc aac gtt aaa gac gca acg gac gcc 451
Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys Asp Ala Thr Asp Ala
105 110 115

acc gaa gca act gtt gca gct gct ttg gaa ctt cct gag ctg acc gac 499
Thr Glu Ala Thr Val Ala Ala Ala Leu Glu Leu Pro Glu Leu Thr Asp
120 125 130

ttc aat cgg ggc aat att aaa gct cgc caa cgc atg gtt gcc cag tac 547
 Phe Asn Arg Gly Asn Ile Lys Ala Arg Gln Arg Met Val Ala Gln Tyr
 135 140 145

 gca atc gca ggc cag ttg ggc ttg ctg gtt att ggc act gat cac gcg 595
 Ala Ile Ala Gly Gln Leu Gly Leu Leu Val Ile Gly Thr Asp His Ala
 150 155 160 165

 gct gaa aac gtc acg ggg ttc ttc acc aaa ttc ggt gat ggc gca gct 643
 Ala Glu Asn Val Thr Gly Phe Phe Thr Lys Phe Gly Asp Gly Ala Ala
 170 175 180

 gac ctg ctt cct ttg gca ggt ttg agc aag cgt caa gga gct gcc att 691
 Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg Gln Gly Ala Ala Ile
 185 190 195

 ctg gag cac ctg ggt gca cct tca agc acg tgg acc aag gtt cct acc 739
 Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp Thr Lys Val Pro Thr
 200 205 210

 gct gat ttg gaa gag gat cgc cca gcg ttg cca gat gag gaa gca ctt 787
 Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro Asp Glu Glu Ala Leu
 215 220 225

 ggt gtg tcg tat gcg gac atc gat aat tac ctg gaa aac aag ccc gat 835
 Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu Glu Asn Lys Pro Asp
 230 235 240 245

 gtc agt gaa aaa gcc cag cag cgc att gag cac ctg tgg aag gtg ggc 883
 Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His Leu Trp Lys Val Gly
 250 255 260

 cag cac aag cgc cac ctc cct gct acc ccg cag gaa aat tgg tgg cgt 931
 Gln His Lys Arg His Leu Pro Ala Thr Pro Gln Glu Asn Trp Trp Arg
 265 270 275

 taatccaaca gtttgagtgt cgc 954

<210> 608

<211> 277

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 608

Met Thr Asn Thr Gln Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro
 1 5 10 15

Ala Ile Asp Val Ala Lys Glu Val Glu Phe Arg Val Gln Phe Leu Val
 20 25 30

Asp Tyr Leu Arg Ala Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser
 35 40 45

Gly Gly Gln Asp Ser Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val
 50 55 60

Glu Arg Ile Arg Ala Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala
 65 70 75 80

Val	Arg	Leu	Pro	Tyr	Ala	Ile	Gln	Ala	Asp	Glu	Asp	Asp	Ala	Gln	Val	
				85	90						95					
Ala	Leu	Glu	Phe	Ile	Ala	Pro	Asp	Lys	Ser	Val	Thr	Val	Asn	Val	Lys	
				100	105						110					
Asp	Ala	Thr	Asp	Ala	Thr	Glu	Ala	Thr	Val	Ala	Ala	Ala	Leu	Glu	Leu	
				115	120						125					
Pro	Glu	Leu	Thr	Asp	Phe	Asn	Arg	Gly	Asn	Ile	Lys	Ala	Arg	Gln	Arg	
				130	135						140					
Met	Val	Ala	Gln	Tyr	Ala	Ile	Ala	Gly	Gln	Leu	Gly	Leu	Leu	Val	Ile	
145				150						155					160	
Gly	Thr	Asp	His	Ala	Ala	Glu	Asn	Val	Thr	Gly	Phe	Phe	Thr	Lys	Phe	
				165	170						175					
Gly	Asp	Gly	Ala	Ala	Asp	Leu	Leu	Pro	Leu	Ala	Gly	Leu	Ser	Lys	Arg	
				180	185						190					
Gln	Gly	Ala	Ala	Ile	Leu	Glu	His	Leu	Gly	Ala	Pro	Ser	Ser	Thr	Trp	
				195	200						205					
Thr	Lys	Val	Pro	Thr	Ala	Asp	Leu	Glu	Glu	Asp	Arg	Pro	Ala	Leu	Pro	
				210	215						220					
Asp	Glu	Glu	Ala	Leu	Gly	Val	Ser	Tyr	Ala	Asp	Ile	Asp	Asn	Tyr	Leu	
225				230						235					240	
Glu	Asn	Lys	Pro	Asp	Val	Ser	Glu	Lys	Ala	Gln	Gln	Arg	Ile	Glu	His	
				245	250						255					
Leu	Trp	Lys	Val	Gly	Gln	His	Lys	Arg	His	Leu	Pro	Ala	Thr	Pro	Gln	
				260	265						270					
Glu	Asn	Trp	Trp	Arg												
275																

```
<210> 609
<211> 1461
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1438)  
<223> RXN02754
```

```

<400> 609
attatgaagc catcggagtt ggtgtggcct acaagggtga tcatgcgtgg atagtgtgtgg 60

agttcactgt agctcccgct gattccgtag aatcaacaga gtg aat acc aat ccg 115
                                     Val Asn Thr Asn Pro
                                     1                               5

tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163
Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr
          10                      15                      20

```

gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc	211
Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg	
25 30 35	
ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga	259
Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg	
40 45 50	
tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac	307
Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp	
55 60 65	
ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac	355
Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp	
70 75 80 85	
cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat	403
Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp	
90 95 100	
ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act	451
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr	
105 110 115	
gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg	499
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu	
120 125 130	
tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg	547
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met	
135 140 145	
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc	595
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg	
150 155 160 165	
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct	643
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala	
170 175 180	
gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att	691
Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile	
185 190 195	
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac	739
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn	
200 205 210	
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa	787
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu	
215 220 225	
tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc	835
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr	
230 235 240 245	
caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca gac ctt ggt ggc	883
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro Asp Leu Gly Gly	
250 255 260	
gta cgt atc gac tcc ggc gac cta ggt gtg ctt gcc cga aag gtc cgc	931

Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg
 265 270 275

aag cag ctc gac gat ctc aac gcc cac aac acc aag att gtg gtc tcc 979
 Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser
 280 285 290

tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt
 1027

Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val
 295 300 305

gac gtc ttt ggc gtt ggc acc tcc gtt gtc aca ggt tct ggc gca cca
 1075

Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro
 310 315 320 325

acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg
 1123

Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val
 330 335 340

gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct
 1171

Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala
 345 350 355

gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac
 1219

Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr
 360 365 370

cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc
 1267

Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser
 375 380 385

ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct
 1315

Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro
 390 395 400 405

act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta
 1363

Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu
 410 415 420

cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act
 1411

Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr
 425 430 435

cgt ttc gtg ggt ttc ccg ccg gcc gct tagacaattc ggtctcacca
 1458

Arg Phe Val Gly Phe Pro Pro Ala Ala
 440 445

aac
 1461

<210> 610
 <211> 446
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 610

Val	Asn	Thr	Asn	Pro	Ser	Glu	Phe	Ser	Ser	Asn	Arg	Ser	Thr	Ala	Leu
1				5					10					15	
Leu	Thr	Asp	Lys	Tyr	Glu	Leu	Thr	Met	Leu	Gln	Ala	Ala	Leu	Ala	Asp
			20					25					30		
Gly	Ser	Ala	Glu	Arg	Pro	Ser	Thr	Phe	Glu	Val	Phe	Ser	Arg	Arg	Leu
		35					40					45			
Pro	Asn	Glu	Arg	Arg	Tyr	Gly	Val	Val	Ala	Gly	Thr	Ala	Arg	Val	Leu
	50					55					60				
Lys	Ala	Ile	Arg	Asp	Phe	Val	Phe	Thr	Glu	Glu	Gln	Leu	Ala	Asp	Leu
65					70					75				80	
Asp	Phe	Leu	Asp	Asp	Arg	Thr	Leu	Glu	Tyr	Leu	Arg	Asn	Tyr	Arg	Phe
				85					90					95	
Thr	Gly	Gln	Val	Asp	Gly	Tyr	Arg	Glu	Gly	Glu	Ile	Tyr	Phe	Pro	Gln
			100					105					110		
Ser	Pro	Leu	Leu	Thr	Val	Arg	Gly	Thr	Phe	Ala	Glu	Cys	Val	Ile	Leu
		115					120					125			
Glu	Thr	Val	Ile	Leu	Ser	Ile	Met	Asn	Ala	Asp	Ser	Ala	Val	Ala	Ser
	130					135						140			
Ala	Ala	Ala	Arg	Met	Val	Thr	Ala	Ala	Asp	Gly	Arg	Pro	Ile	Ile	Glu
145					150					155					160
Met	Gly	Ser	Arg	Arg	Thr	His	Glu	Tyr	Ser	Ala	Val	Thr	Ala	Ser	Arg
				165					170					175	
Ala	Ala	Tyr	Leu	Ala	Gly	Phe	Ser	Thr	Thr	Ser	Asn	Leu	Glu	Ala	Ala
			180					185					190		
Tyr	Arg	Tyr	Gly	Ile	Pro	Ala	Ser	Gly	Thr	Ser	Ala	His	Ala	Tyr	Thr
			195					200					205		
Leu	Leu	His	Ile	Asn	Asp	Asp	Gly	Thr	Pro	Asn	Glu	Ala	Ala	Ala	Phe
	210					215					220				
Lys	Ala	Gln	Val	Glu	Ser	Leu	Gly	Val	Asp	Thr	Thr	Leu	Leu	Val	Asp
225					230					235				240	
Thr	Tyr	Asp	Ile	Thr	Gln	Gly	Val	Ala	Thr	Ala	Ile	Glu	Val	Ala	Gly
			245						250					255	
Pro	Asp	Leu	Gly	Gly	Val	Arg	Ile	Asp	Ser	Gly	Asp	Leu	Gly	Val	Leu
		260						265					270		
Ala	Arg	Lys	Val	Arg	Lys	Gln	Leu	Asp	Asp	Leu	Asn	Ala	His	Asn	Thr
		275					280					285			
Lys	Ile	Val	Val	Ser	Ser	Asp	Leu	Asp	Glu	Phe	Ala	Ile	Ala	Gly	Leu

290	295	300
Arg Gly Glu Pro Val	Asp Val Phe Gly Val	Gly Thr Ser Val Val Thr
305	310	315 320
Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val		
	325	330 335
Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly		
	340	345 350
Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile		
	355	360 365
Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys		
	370	375 380
Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile		
	385	390 395 400
Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys		
	405	410 415
Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu		
	420	425 430
Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro Ala Ala		
	435	440 445

<210> 611

<211> 531

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(508)

<223> RXA02299

<400> 611

acgcgggggt tgttgccgga tcgaaatatt cctttccttg tcattctcag ctagatttc 60

taaaacttgc	aggacaaccc	ccataaggac	accacaggac	atg ctg cgc acc atc	115
				Met Leu Arg Thr Ile	
				1 5	

ctc gga agt aag att cac cga gcc act gtc act caa gct gat cta gat	163
Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr Gln Ala Asp Leu Asp	
10 15 20	

tat gtt ggc tct gta acc atc gac gcc gac ctg gtt cac gcc gcc gga	211
Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu Val His Ala Ala Gly	
25 30 35	

ttg atc gaa ggc gaa aaa gtt gcc atc gta gac atc acc aac ggc gct	259
Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp Ile Thr Asn Gly Ala	
40 45 50	

cgt ctg gaa act tat gtc att gtg ggc gac gcc gga acg ggc aat att	307
Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala Gly Thr Gly Asn Ile	


```

<400> 612
Met Leu Arg Thr Ile Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr
  1             5             10             15
Gln Ala Asp Leu Asp Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu
      20             25             30
Val His Ala Ala Gly Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp
      35             40             45
Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala
  50             55             60
Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn
  65             70             75             80

```

```
<210> 613
<211> 960
<212> DNA
<213> Corynebacterium glutamicum
```

<220>

<221> CDS

<222> (101)..(937)

<223> RXA01928

<400> 613

gcgagtagcg caccttgggc gattccttgc acgacgccgc gcaggcctac atcgccgata 60

tccacgcggg taccttccca ggcgaagcgg agtcctttta atg cag gta gca acc 115
 Met Gln Val Ala Thr
 1 5

aca aag cag gcg ctt atc gac gcc ctc ctc cac cac aaa tcc gtc ggg 163
 Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His His Lys Ser Val Gly
 10 15 20

ctc gtc ccc acc atg ggt gcg cta cac agc gga cac gcc tcg ttg gtt 211
 Leu Val Pro Thr Met Gly Ala Leu His Ser Gly His Ala Ser Leu Val
 25 30 35

aaa gca gca cgc gct gaa aac gac act gtt gta gcc agt att ttt gtc 259
 Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val Ala Ser Ile Phe Val
 40 45 50

aat ccc ctg cag ttt gaa gca ctc ggt gat tgc gat gat tac cgc aac 307
 Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys Asp Asp Tyr Arg Asn
 55 60 65

tat ccc cgc caa ctc gac gcc gat tta gca ctg ctt gaa gag gca ggt 355
 Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu Leu Glu Glu Ala Gly
 70 75 80 85

gtg gat att gtg ttc gca ccc gat gtg gag gaa atg tac ccc ggt ggc 403
 Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu Met Tyr Pro Gly Gly
 90 95 100

ttg cca cta gtg tgg gcg cgc acc ggt tcc atc gga aca aaa ttg gag 451
 Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile Gly Thr Lys Leu Glu
 105 110 115

ggt gcc agc agg cct ggc cat ttc gat ggt gtg gct acc gtg gtg gcg 499
 Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val Ala Thr Val Val Ala
 120 125 130

aag ctg ttc aat ttg gtg cgc cct gat cgt gca tat ttt gga caa aaa 547
 Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala Tyr Phe Gly Gln Lys
 135 140 145

gat gct cag cag gtt gcg gtg att cgg cga ttg gtt gcc gat cta gac 595
 Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu Val Ala Asp Leu Asp
 150 155 160 165

att ccc gtg gag att cgt ccc gtt ccg att att cgt ggc gcc gat ggc 643
 Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile Arg Gly Ala Asp Gly
 170 175 180

tta gcc gaa tcc agc cgc aat caa cgt ctt tct gcg gat cag cga gcg 691
 Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser Ala Asp Gln Arg Ala
 185 190 195

caa gct ctg gtg ctg ccg cag gtg ttg agt ggg ttg cag cgt cga aaa 739
 Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly Leu Gln Arg Arg Lys
 200 205 210

gca gct ggt gaa gcg cta gat atc caa ggt gcg cgc gac acc ttg gcc 787
 Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala Arg Asp Thr Leu Ala
 215 220 225

agc gcc gac ggc gtg cgc ttg gat cac ctg gaa att gtc gat cca gcc 835
 Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu Ile Val Asp Pro Ala
 230 235 240 245

acc ctc gaa cca tta gaa atc gac ggc ctg ctc acc caa cca gcg ttg 883
 Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu Thr Gln Pro Ala Leu
 250 255 260

gtg gtc ggc gcg att ttc gtg ggg ccg gtg cgg ttg atc gac aat atc 931
 Val Val Gly Ala Ile Phe Val Gly Pro Val Arg Leu Ile Asp Asn Ile
 265 270 275

gag ctc tagtaccac cctgcgttgc agc 960
 Glu Leu

<210> 614

<211> 279

<212> PRT

<213> Corynebacterium glutamicum

<400> 614

Met Gln Val Ala Thr Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His
 1 5 10 15

His Lys Ser Val Gly Leu Val Pro Thr Met Gly Ala Leu His Ser Gly
 20 25 30

His Ala Ser Leu Val Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val
 35 40 45

Ala Ser Ile Phe Val Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys
 50 55 60

Asp Asp Tyr Arg Asn Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu
 65 70 75 80

Leu Glu Glu Ala Gly Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu
 85 90 95

Met Tyr Pro Gly Gly Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile
 100 105 110

Gly Thr Lys Leu Glu Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val
 115 120 125

Ala Thr Val Val Ala Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala
 130 135 140

Tyr Phe Gly Gln Lys Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu
 145 150 155 160

Val Ala Asp Leu Asp Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile
165 170 175

Arg Gly Ala Asp Gly Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser
180 185 190

Ala Asp Gln Arg Ala Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly
195 200 205

Leu Gln Arg Arg Lys Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala
210 215 220

Arg Asp Thr Leu Ala Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu
225 230 235 240

Ile Val Asp Pro Ala Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu
245 250 255

Thr Gln Pro Ala Leu Val Val Gly Ala Ile Phe Val Gly Pro Val Arg
260 265 270

Leu Ile Asp Asn Ile Glu Leu
275

<210> 615

<211> 936

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(913)

<223> RXN01929

<400> 615

aaaatttgac tccataacga gaacttaatc gagcaacacc cctgaacagt gaatcaaac 60

ggaatttatt tattctgagc tggatcatcac atctatactc atg ccc atg tca ggc 115
Met Pro Met Ser Gly
1 5

att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta 163
Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val
10 15 20

aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211
Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala
25 30 35

cgc att ttt qat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc 259
Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser
40 45 50

gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg 307
Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu
55 60 65

gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt 355
Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg
70 75 80 85

gcg ctt gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca 403
 Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro
 90 95 100

aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg 451
 Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala
 105 110 115

gct gcg gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga 499
 Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg
 120 125 130

cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc 547
 Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr
 135 140 145

ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc 595
 Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly
 150 155 160 165

gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg 643
 Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala
 170 175 180

ggt gcg ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc 691
 Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg
 185 190 195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739
 Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly
 200 205 210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787
 Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu
 215 220 225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835
 Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly
 230 235 240 245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883
 Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala
 250 255 260

ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca 933
 Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 265 270

aag 936

<210> 616

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 616

Met Pro Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe
 1 5 10 15

Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr
 20 25 30
 Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu
 35 40 45
 Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr
 50 55 60
 Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr
 65 70 75 80
 Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr
 85 90 95
 Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met
 100 105 110
 Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile
 115 120 125
 Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly
 130 135 140
 His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val
 145 150 155 160
 Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg
 165 170 175
 Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro
 180 185 190
 Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile
 195 200 205
 Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln
 210 215 220
 Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu
 225 230 235 240
 Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile
 245 250 255
 Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 260 265 270

<210> 617

<211> 930

<212> --IA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(907)

<223> FRXA01929

<400> 617

tgactccata acgagaactt aatcgagcaa cacccttgaa cagtgaatca aatcggaatt 60

tatttattct gagctgggtca tcacatctat actcatgccc atg tca ggc att gat	115
Met Ser Gly Ile Asp	
1 5	
gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc	163
Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly	
10 15 20	
cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att	211
Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile	
25 30 35	
ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc	259
Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala	
40 45 50	
aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag	307
Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu	
55 60 65	
atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt	355
Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg Ala Leu	
70 75 80 85	
gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca aat cag	403
Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro Asn Gln	
90 95 100	
gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg gct gcg	451
Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala Ala Ala	
105 110 115	
gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga cgc att	499
Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg Arg Ile	
120 125 130	
gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc ccg cag	547
Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr Pro Gln	
135 140 145	
tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc gcg agt	595
Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly Ala Ser	
150 155 160 165	
tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg ggt gcg	643
Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala Gly Ala	
170 175 180	
ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc gag gtt	691
Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg Glu Val	
185 190 195	
acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc aat ggc	739
Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly Asn Gly	
200 205 210	
aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc aac cgc	787
Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu Asn Arg	
215 220 225	

ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc gat tcc 835
 Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly Asp Ser
 230 235 240 245

ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg ggt acc 883
 Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala Gly Thr
 250 255 260

ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca aag 930
 Phe Pro Gly Glu Ala Glu Ser Phe
 265

<210> 618

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 618

Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu
 1 5 10 15

Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala
 20 25 30

Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val
 35 40 45

Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser
 50 55 60

Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala
 65 70 75 80

Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu
 85 90 95

Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu
 100 105 110

Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln
 115 120 125

Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile
 130 135 140

Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln
 145 150 155 160

Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu
 165 170 175

Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu
 180 185 190

Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile
 195 200 205

Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala
 210 215 220

Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala
225 230 235 240

Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp
245 250 255

Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
260 265

<210> 619

<211> 921

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(898)

<223> RXA01521

<400> 619

accccggcag gcaacgcctt ttccgggatt tggcgcgag gcaggcagag atttcccgcg 60

cgcaagatat tgagctgtgg gcaattcaga aggaggaccg ttg agt ttc acg cat 115
Leu Ser Phe Thr His
1 5

ggg cag ggc aga gtt ttt gat acc gtc gag cag atc cgc atg ttc ggc 163
Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln Ile Arg Met Phe Gly
10 15 20

agc gcc ctg cgc aaa acc ggc aaa cca gtg gtg ctc gta ccc ttg gga 211
Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val Leu Val Pro Leu Gly
25 30 35

aat ggc ctc cac gca ggc cat att gcg ctc atc cgc gca gca aaa cgc 259
Asn Gly Leu His Ala Gly His Ile Ala Leu Ile Arg Ala Ala Lys Arg
40 45 50

atc ccc ggt gcg gtg gtc gtc gtc gcc tat gcc ggc ccg gaa tcg gat 307
Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala Gly Pro Glu Ser Asp
55 60 65

cac gca cgt tta agg gaa gag ctt atc gac gcg atc ttc ccg ttc aat 355
His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala Ile Phe Pro Phe Asn
70 75 80 85

ccc gaa acg cta tgg cct cac ggc atc cgg gtg gaa gtt aca ggt ggc 403
Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val Glu Val Thr Gly Gly
90 95 100

cca aca ctt acc cca caa ggt gcg gaa gta acc aag gtg ctg ggg ctg 451
Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr Lys Val Leu Gly Leu
105 110 115

ttg gga atc acc gga gca act gat gtg gtg ctc ggt gaa aag gac tat 499
Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu Gly Glu Lys Asp Tyr
120 125 130

gag ctg gtg gtt cta gtc cag cgc gcc ctt aat gat ctg cat att cca 547
Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn Asp Leu His Ile Pro

135	140	145	
gta aaa ctg cat tct gtt cca acc gtg cgc atg cca gat gga cta gcc			595
Val Lys Leu His Ser Val Pro Thr Val Arg Met Pro Asp Gly Leu Ala			
150	155	160	165
att tcc ctg cgt aat att tca gtg ccc gaa gac tcc cgc gaa acg gca			643
Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp Ser Arg Glu Thr Ala			
170	175		180
ttg agc ctg gca gca gcc ctc acc gcc ggt gcg cat tcg gca gaa cac			691
Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala His Ser Ala Glu His			
185	190		195
ggc gag gca gtg gtt aaa gaa aca gtc acg caa gtg ctc aaa gcc gca			739
Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln Val Leu Lys Ala Ala			
200	205		210
ggc gtg acc ccc gat tat gta gaa atc cgc ggc ctg gat ctt gga cca			787
Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly Leu Asp Leu Gly Pro			
215	220		225
gcc ccc gaa atc gga gac gcc cga ctc ttc gca gcc atc acg ctt ggc			835
Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala Ala Ile Thr Leu Gly			
230	235		240
gat gtc caa ctc cac gac aac gtc ggc cta ccc ctt gga atc ggc ttc			883
Asp Val Gln Leu His Asp Asn Val Gly Leu Pro Leu Gly Ile Gly Phe			
250	255		260
aaa aac atc gaa ggc tgatcccggt ttacccagtt cgc			921
Lys Asn Ile Glu Gly			
265			

<210> 620

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 620

Leu Ser Phe Thr His Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln
1 5 10 15

Ile Arg Met Phe Gly Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val
20 25 30

Leu Val Pro Leu Gly Asn Gly Leu His Ala Gly His Ile Ala Leu Ile
35 40 45

Arg Ala Ala Lys Arg Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala
50 55 60

Gly Pro Glu Ser Asp His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala
65 70 75 80

Ile Phe Pro Phe Asn Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val
85 90 95

Glu Val Thr Gly Gly Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr
100 105 110

Lys Val Leu Gly Leu Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu
 115 120 125
 Gly Glu Lys Asp Tyr Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn
 130 135 140
 Asp Leu His Ile Pro Val Lys Leu His Ser Val Pro Thr Val Arg Met
 145 150 155 160
 Pro Asp Gly Leu Ala Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp
 165 170 175
 Ser Arg Glu Thr Ala Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala
 180 185 190
 His Ser Ala Glu His Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln
 195 200 205
 Val Leu Lys Ala Ala Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly
 210 215 220
 Leu Asp Leu Gly Pro Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala
 225 230 235 240
 Ala Ile Thr Leu Gly Asp Val Gln Leu His Asp Asn Val Gly Leu Pro
 245 250 255
 Leu Gly Ile Gly Phe Lys Asn Ile Glu Gly
 260 265

<210> 621
 <211> 1137
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1114)
 <223> RXS01145

<400> 621

taatgtagtt gtctgcccaa gcgagttaaa ctcccacgat ttacagtggg gggcagacat 60
 cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct	307
Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala	
55 60 65	
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc	355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr	
70 75 80 85	
tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca	403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala	
90 95 100	
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg	451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	
105 110 115	
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc	499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly	
120 125 130	
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct	547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro	
135 140 145	
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg	595
Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu	
150 155 160 165	
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc	643
Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile	
170 175 180	
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag	691
Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln	
185 190 195	
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag	739
Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu	
200 205 210	
ggt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt	787
Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val	
215 220 225	
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc	835
Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile	
230 235 240 245	
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac	883
Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr	
250 255 260	
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag	931
Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys	
265 270 275	
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc	979
Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile	
280 285 290	

gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc
1027

Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser
295 300 305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc
1075

Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu
310 315 320 325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac
1124

Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala
330 335

ccctttgacg gct
1137

<210> 622

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 622

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
130 135 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly
145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
180 185 190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
 195 200 205

Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met
 210 215 220

Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
 225 230 235 240

Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
 245 250 255

Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr
 260 265 270

Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe
 275 280 285

Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu
 290 295 300

Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala
 305 310 315 320

Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu
 325 330 335

Thr Ala

<210> 623

<211> 556

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> FRXA01145

<400> 623

taatgtagtt gtctgcccac gcgagttaaa ctcccacgat ttacagtggg gggcagacat 60

cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala
 55 60 65

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355
 Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr
 70 75 80 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403
 Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala
 90 95 100

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451
 Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu
 105 110 115

atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499
 Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly
 120 125 130

cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547
 Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro
 135 140 145

tgc ctc atc 556
 Cys Leu Ile
 150

<210> 624

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 624

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
 1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
 20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
 35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
 50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
 65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
 85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
 100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
 115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
 130 135 140

Gly Lys Gly Val Pro Cys Leu Ile
145 150

<210> 625
<211> 1389
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1366)
<223> RXA02239

<400> 625
ctatgcacag cggaggtcga gggagagcgt ggggtggcgt cgaaaagcat cttgtagagt 60
gtgtgggaac ccagccagcc tcttactttg aaggattgtt gtg ccc atg act cat 115
Val Pro Met Thr His
1 5
gtt tca agc ccc tcc gca ccc cgc aac gtg gtt gtt ggt gtt gcc ggc 163
Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val Val Gly Val Ala Gly
10 15 20
gga atc gca gcg tac aag gcg tgt cac atc gtg cgc gcg ttt aaa gaa 211
Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val Arg Ala Phe Lys Glu
25 30 35
gcg ggc gat aat gtg cgg gtg gtt cct acg gaa tcc gcg ttg aag ttt 259
Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu Ser Ala Leu Lys Phe
40 45 50
gtg ggg aag gcg acg ttt gaa gcg ttg tct ggc aat ccg gtg tct aca 307
Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly Asn Pro Val Ser Thr
55 60 65
acg gtg ttt gat gcg gtg gat tcc gtg cag cat gtg aaa gtt ggc cag 355
Thr Val Phe Asp Ala Val Asp Ser Val Gln His Val Lys Val Gly Gln
70 75 80 85
gaa gct gat ttg atc gtg att gcg ccg gcg aca gcc gat ttg atg gcg 403
Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr Ala Asp Leu Met Ala
90 95 100
cgt gtg gtg gca ggt ctc ggt gac gat ctg ttg gcg gcg acg ctg ctg 451
Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu Ala Ala Thr Leu Leu
105 110 115
gtg gca acg tgc ccc gtg gtt att gcg ccg gcc atg cat acg gag atg 499
Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala Met His Thr Glu Met
120 125 130
tgg ttt aat ccg gct acc gta gcc aat gtg gca acg ctg agg cag cgg 547
Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala Thr Leu Arg Gln Arg
135 140 145
ggg att acc gtg att gag cct gcg cat ggt cga ctc acc ggt aaa gat 595
Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg Leu Thr Gly Lys Asp
150 155 160 165

aca ggc cct ggc cgg ctg ccg gat cca gag cag att gtt gat tta gcc 643
 Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln Ile Val Asp Leu Ala
 170 175 180

aat gcg gtg cac gcc ggg gcg agg ttg cct cag gat ttg gcg ggc aag 691
 Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln Asp Leu Ala Gly Lys
 185 190 195

aaa gtg ctg atc act gct ggt ggc acg cat gag cat att gat cct gtg 739
 Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu His Ile Asp Pro Val
 200 205 210

cgc ttt att ggc aat agt tcc tcg ggc cgt caa ggt ttt gcg ttg ggt 787
 Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln Gly Phe Ala Leu Gly
 215 220 225

gaa atc gca gca cag cga ggt gct cat gtc agc atc gtg gcg gga aat 835
 Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser Ile Val Ala Gly Asn
 230 235 240 245

gct gcg gag ctg ccc act ccg gca ggc gca gag atc gtg ccg gtg gtg 883
 Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu Ile Val Pro Val Val
 250 255 260

tcc aca caa gac atg ttt gat gca gtc cag gaa cga gct ggc caa tct 931
 Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu Arg Ala Gly Gln Ser
 265 270 275

gat ttc atc gtc atg gcg gca gcg gta gct gat ttc acg ccc gca tcg 979
 Asp Phe Ile Val Met Ala Ala Val Ala Asp Phe Thr Pro Ala Ser
 280 285 290

cag gcg aca tcg aag ttg aag aag ggc tca gat tct gat gaa gac gca
 1027
 Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp Ser Asp Glu Asp Ala
 295 300 305

ttg agc acc atc tcg ttg gtg gaa aac ccg gat att ttg gct acc acg
 1075
 Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp Ile Leu Ala Thr Thr
 310 315 320 325

gtg aag cgt cgt gaa gca gga gac ctg gac agt aat cct gtc atc gtc
 1123
 Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser Asn Pro Val Ile Val
 330 335 340

ggt ttt gct gcg gaa act gga gac gag cac acc acc gcc ttg gag tat
 1171
 Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr Thr Ala Leu Glu Tyr
 345 350 355

gcg cgc aag aaa ctg cag aag aag ggc tgc gac ctc ctc atg tgt aat
 1219
 Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp Leu Leu Met Cys Asn
 360 365 370

gag gtg ggc atg ggc aaa gtg ttt ggg caa aag cac aat gag ggc tgg
 1267
 Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys His Asn Glu Gly Trp
 375 380 385

att ttg gat gct cac ggt ggg gta gtc gat gtg gag cac ggc agc aaa
1315

Ile Leu Asp Ala His Gly Gly Val Val Asp Val Glu His Gly Ser Lys
390 395 400 405

atc gag gtt gct gcg caa att tgg gac gcg gca ctg gcg tat cgc gaa
1363

Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala Leu Ala Tyr Arg Glu
410 415 420

gtc tagaaaaatc cagctagacc act

1389

Val

<210> 626

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 626

Val Pro Met Thr His Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val
1 5 10 15

Val Gly Val Ala Gly Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val
20 25 30

Arg Ala Phe Lys Glu Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu
35 40 45

Ser Ala Leu Lys Phe Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly
50 55 60

Asn Pro Val Ser Thr Thr Val Phe Asp Ala Val Asp Ser Val Gln His
65 70 75 80

Val Lys Val Gly Gln Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr
85 90 95

Ala Asp Leu Met Ala Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu
100 105 110

Ala Ala Thr Leu Leu Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala
115 120 125

Met His Thr Glu Met Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala
130 135 140

Thr Leu Arg Gln Arg Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg
145 150 155 160

Leu Thr Gly Lys Asp Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln
165 170 175

Ile Val Asp Leu Ala Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln
180 185 190

Asp Leu Ala Gly Lys Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu
195 200 205

His Ile Asp Pro Val Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln
 210 215 220
 Gly Phe Ala Leu Gly Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser
 225 230 235 240
 Ile Val Ala Gly Asn Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu
 245 250 255
 Ile Val Pro Val Val Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu
 260 265 270
 Arg Ala Gly Gln Ser Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp
 275 280 285
 Phe Thr Pro Ala Ser Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp
 290 295 300
 Ser Asp Glu Asp Ala Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp
 305 310 315 320
 Ile Leu Ala Thr Thr Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser
 325 330 335
 Asn Pro Val Ile Val Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr
 340 345 350
 Thr Ala Leu Glu Tyr Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp
 355 360 365
 Leu Leu Met Cys Asn Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys
 370 375 380
 His Asn Glu Gly Trp Ile Leu Asp Ala His Gly Gly Val Val Asp Val
 385 390 395 400
 Glu His Gly Ser Lys Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala
 405 410 415
 Leu Ala Tyr Arg Glu Val
 420

<210> 627
 <211> 1092
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1069)
 <223> RXA00581

<400> 627
 gcatgagttt actcacgtgc ccacgtcttt tagccaccca ttgaagtga aaaataaccc 60
 cgatcacact agtggagtag ctaaggtgca caatggattc atg gca gag caa aac 115
 Met Ala Glu Gln Asn
 1 5

gct gca agc aca act ggt gtg aaa cct tcc cca cgc aca cca gat ttc	163
Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro Arg Thr Pro Asp Phe	
10 15 20	
agc ccc tac ctt gat ttc gac cgc gca caa tgg cgc gag ctg aga aac	211
Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp Arg Glu Leu Arg Asn	
25 30 35	
tca atg cct cag gtg ctg acc caa aaa gaa gtc att gaa ctt cga ggc	259
Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val Ile Glu Leu Arg Gly	
40 45 50	
atc gga gaa aac att gac ctc gct gaa gtg gca gaa gtc tac ctt ccg	307
Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala Glu Val Tyr Leu Pro	
55 60 65	
ctg tcc cgt ctg att cac ctc cag gta gcg gcc cga cag caa ctt act	355
Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala Arg Gln Gln Leu Thr	
70 75 80 85	
gca gcc acc gaa acc ttc ctc gga act tcc ccc tct atc tct gtg ccg	403
Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro Ser Ile Ser Val Pro	
90 95 100	
ttt gtc att ggt gtc gcg gga tcc gtc gcc gtc ggt aaa tca acc acc	451
Phe Val Ile Gly Val Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr	
105 110 115	
gcc cga ctc ctc caa gtt ctg ctt cag cgc tgg aat tcc cac ccc cgc	499
Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp Asn Ser His Pro Arg	
120 125 130	
gtg gac ctc gtc acc acc gac gga ttc ctc tat ccc gcc gcg gaa cta	547
Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr Pro Gly Ala Glu Leu	
135 140 145	
atc cgc cgc gga tta atg tcc cga aaa gga ttc ccc gaa agc tac gac	595
Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe Pro Glu Ser Tyr Asp	
150 155 160 165	
caa cgt gca ctc ctc cgc ttt gtc acc gac gta aaa tcc gga aaa ctc	643
Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val Lys Ser Gly Lys Leu	
170 175 180	
gaa gtc aac gca cct gtc tac tcc cac acc gcg tac gac cga gtt cca	691
Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala Tyr Asp Arg Val Pro	
185 190 195	
ggc gaa ttc acc aca gtc cgc caa ccc gac att ttg atc gtc gaa ggc	739
Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile Leu Ile Val Glu Gly	
200 205 210	
tta aac gtc ctc caa act ggc cca aca ttg atg gtc agt gac ctt ttc	787
Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met Val Ser Asp Leu Phe	
215 220 225	
gac ttc agc gtc tac gta gat gcc cgc acc gaa gat atc gaa aaa tgg	835
Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu Asp Ile Glu Lys Trp	
230 235 240 245	
tac atc gac cgc ttc ctc aaa ctc cgc gac act gca ttc cgt cgc ccc	883

Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr Ala Phe Arg Arg Pro
 250 255 260
 ggt gcc cac ttc tcc cat tac gcc gac atg gct gat cca gag tcc atc 931
 Gly Ala His Phe Ser His Tyr Ala Asp Met Ala Asp Pro Glu Ser Ile
 265 270 275
 gcc gtc gct cga gaa ctg tgg caa tcg atc aac ctg ccc aac ttg gtg 979
 Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn Leu Pro Asn Leu Val
 280 285 290
 gag aat att ctt ccc acc cga gtt cgc gcg tcg ttg gta ctg aaa aaa
 1027
 Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser Leu Val Leu Lys Lys
 295 300 305
 ggt agc gat cac ttg gtg gaa cgg gtg agg atg cgc aag atc
 1069
 Gly Ser Asp His Leu Val Glu Arg Val Arg Met Arg Lys Ile
 310 315 320
 taggggttct tgctgggttt gag
 1092

<210> 628
 <211> 323
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 628
 Met Ala Glu Gln Asn Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro
 1 5 10 15
 Arg Thr Pro Asp Phe Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp
 20 25 30
 Arg Glu Leu Arg Asn Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val
 35 40 45
 Ile Glu Leu Arg Gly Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala
 50 55 60

Glu Val Tyr Leu Pro Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala
 65 70 75 80
 Arg Gln Gln Leu Thr Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro
 85 90 95
 Ser Ile Ser Val Pro Phe Val Ile Gly Val Ala Gly Ser Val Ala Val
 100 105 110
 Gly Lys Ser Thr Thr Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp
 115 120 125
 Asn Ser His Pro Arg Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr
 130 135 140
 Pro Gly Ala Glu Leu Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe
 145 150 155 160

Pro Glu Ser Tyr Asp Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val
 165 170 175

Lys Ser Gly Lys Leu Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala
 180 185 190

Tyr Asp Arg Val Pro Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile
 195 200 205

Leu Ile Val Glu Gly Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met
 210 215 220

Val Ser Asp Leu Phe Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu
 225 230 235 240

Asp Ile Glu Lys Trp Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr
 245 250 255

Ala Phe Arg Arg Pro Gly Ala His Phe Ser His Tyr Ala Asp Met Ala
 260 265 270

Asp Pro Glu Ser Ile Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn
 275 280 285

Leu Pro Asn Leu Val Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser
 290 295 300

Leu Val Leu Lys Lys Gly Ser Asp His Leu Val Glu Arg Val Arg Met
 305 310 315 320

Arg Lys Ile

<210> 629
 <211> 1023
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1000)
 <223> RXS00838

<400> 629
 tcgtctaata gtgctgccaa tccaccggcc attgatgact cctttgtaga gaaggggtag 60

tgcttacaaa tcttatctgt gctcaggcaa gatagcaggt atg aaa att gcg atc 115
 Met Lys Ile Ala Ile
 1 5

gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163
 Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu
 10 15 20

tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc 211
 Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala
 25 30 35

ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac 259
 Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr

40	45	50	
gta cca att cct gca gtt gcg agc gtg caa gaa cta aaa gat gca gat			307
Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu Leu Lys Asp Ala Asp			
55	60	65	
gta gtg atg att gct act aaa gca tta tcg cgg tct tta gat ctc gct			355
Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg Ser Leu Asp Leu Ala			
70	75	80	85
gaa ctt ttg ggt ggg ata cct gcg aat tcg gtg gtc gcg att act cag			403
Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val Val Ala Ile Thr Gln			
	90	95	100
aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat			451
Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp			
	105	110	115
cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca			499
Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro			
	120	125	130
gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat			547
Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp			
	135	140	145
tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt			595
Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly			
150	155	160	165
att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa			643
Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys			
	170	175	180
gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag			691
Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys			
	185	190	195
caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg			739
Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu			
	200	205	210
atg gaa gag gtg gct gag gtg gct cgc gag gaa ggt gtt gag ttc cgc			787
Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro			
	215	220	225
agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag			835
Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu			
230	235	240	245
aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt			883
Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser			
	250	255	260
gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg			931
Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val			
	265	270	275
ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg			979
Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu			
	280	285	290

aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg

1023

Lys Glu Glu Glu Asn Ser Leu
295 300

<210> 630

<211> 300

<212> PRT

<213> Corynebacterium glutamicum

<400> 630

Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly
1 5 10 15

Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly
20 25 30

Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala
35 40 45

Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu
50 55 60

Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg
65 70 75 80

Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val
85 90 95

Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys
100 105 110

Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe
115 120 125

Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser
130 135 140

Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr
145 150 155 160

Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val
165 170 175

Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly
180 185 190

Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala
195 200 205

Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala
210 215 220

Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala
225 230 235 240

Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala
245 250 255

Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg
260 265 270

Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr
275 280 285

Ala Gly Leu Lys Leu Lys Glu Glu Glu Asn Ser Leu
290 295 300

<210> 631

<211> 408

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(385)

<223> RXC02238

<400> 631

ggcgcttagc caaaacatag agcggtaggg tatgcttatt cgattgagca acctttcccg 60

ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115
Val Thr Asn Val Ser
1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
25 30 35

gcc ctg gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
40 45 50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
55 60 65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
70 75 80 85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
90 95

cac 408

<210> 632

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 632

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp

1	5	10	15
Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys			
20	25	30	
Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg			
35	40	45	
Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe			
50	55	60	
Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile			
65	70	75	80
Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly			
85	90	95	

<210> 633
 <211> 606
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(583)
 <223> RXN03058

<400> 633
 acgagcttcc gctctgcaca agccgctaga agcccgcat agccctaagt tagagctcat 60

gcccatttgg aatcacaaca ccgcatatcg gccatggctg gtg tca aag ctc aaa 115
 Val Ser Lys Leu Lys
 1 5

ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163
 Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala
 10 15 20

gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211
 Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu
 25 30 35

att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259
 Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala
 40 45 50

atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307
 Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu
 55 60 65

aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355
 Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val
 70 75 80 85

ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403
 Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu
 90 95 100

caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451
 Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln

105 110 115
 atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata 499
 ile tyr pro phe pro thr lys glu pro ser glu ser leu his glu ile
 120 125 130
 cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga 547
 arg gln leu thr lys gln leu leu pro his arg arg ile arg arg gly
 135 140 145
 atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc 593
 ile his phe arg tyr leu leu glu trp thr lys pro
 150 155 160
 tataaaccaa aaa 606

<210> 634
 <211> 161
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 634
 Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly
 1 5 10 15
 Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp
 20 25 30
 Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr
 35 40 45
 Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn
 50 55 60
 Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly
 65 70 75 80
 Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp
 85 90 95
 ile ile ser gly leu gln ala phe leu ser arg pro ile ser leu ile
 100 105 110

Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu
 115 120 125
 Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg
 130 135 140
 Arg ile arg arg gly ile his phe arg tyr leu leu glu trp thr lys
 145 150 155 160
 Pro

<210> 635
 <211> 606
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(583)

<223> FRXA02903

<400> 635

acgagcttcc gctctgcaca agccgctaga agccccgcat agccctaattg tagagctcat 60

gccccatttg aatcacaaca ccgcataatcg gccatggctg gtg tca aag ctc aaa 115
 Val Ser Lys Leu Lys
 1 5

ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163
 Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala
 10 15 20

gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211
 Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu
 25 30 35

att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259
 Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala
 40 45 50

atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307
 Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu
 55 60 65

aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355
 Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val
 70 75 80 85

ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403
 Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu
 90 95 100

caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451
 Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln
 105 110 115

atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata 499
 Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile
 120 125 130

cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga 547
 Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly
 135 140 145

atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc 593
 Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro
 150 155 160

tataaaccaa aaa 606

<210> 636

<211> 161

<212> PRT

<213> Corynebacterium glutamicum

<400> 636

Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly
 1 5 10 15

Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp
 20 25 30

Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr
 35 40 45

Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn
 50 55 60

Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly
 65 70 75 80

Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp
 85 90 95

Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile
 100 105 110

Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu
 115 120 125

Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg
 130 135 140

Arg Ile Arg Arg Gly Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys
 145 150 155 160

Pro

<210> 637

<211> 783

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) - (760)

<223> RXA00166

<400> 637

ggcgttttagc gatcttcaac atcgagcaac cagcgccagc gctttttaccc aaggcagcac 60

gacttatcac gatgtccgac ctggatatcc ggctgaggcc gtg gag tta gcc cgt 115
 Val Glu Leu Ala Arg
 1 5

ggg ttt ggc cga gtc ctg gat gtc ggt gca ggt acc gga aaa cta acc 163
 Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr
 10 15 20

agt gag cta aca gct gat cag gtc cta gcc ctt gat cca agc atg gac 211
 Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu Asp Pro Ser Met Asp
 25 30 35

atg ttg cgg gtg ttt cgc tcc gcg ctt ccg gcg gtt ccc tgc tgg caa 259

Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala Val Pro Cys Trp Gln
 40 45 50

gcg aca gca gaa cac aca gga ata cgt gac aac gcg gtt gat ctg att 307
 Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn Ala Val Asp Leu Ile
 55 60 65

acg tgc gca caa acg tgg cat tgg gtt gac gtg acg gct gcc tca gcg 355
 Thr Cys Ala Gln Thr Trp His Trp Val Asp Val Thr Ala Ala Ser Ala
 70 75 80 85

gaa ttt gat cgg gtg att gca cct gag ggt gca gtc ctg ctc gtg tgg 403
 Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala Val Leu Leu Val Trp
 90 95 100

aat aac ctg gac acc tcc atc gcg tgg gta cac cga ctc agt cgc att 451
 Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His Arg Leu Ser Arg Ile
 105 110 115

atg cat gcc ggc gat gta ctc aag ccg gga ttc acc cca gaa acc gca 499
 Met His Ala Gly Asp Val Leu Lys Pro Gly Phe Thr Pro Glu Thr Ala
 120 125 130

gct ccc tgg ata att gat cga gaa att cgc acc acg tgg aat cag cac 547
 Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr Thr Trp Asn Gln His
 135 140 145

ctc acc cct gaa gaa atc atc cag ctc gct cac acg agg tcc tac tgg 595
 Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His Thr Arg Ser Tyr Trp
 150 155 160 165

tta aac gcg tca gag aaa atc aaa gag cgt gtt gat cag aac ctt cag 643
 Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val Asp Gln Asn Leu Gln
 170 175 180

tgg tat ctc tac gag cat ttg ggt ttc agt ccc gac aat cca gtg gaa 691
 Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro Asp Asn Pro Val Glu
 185 190 195

ctt ccc tat cgc tgt gat gca ttt tta ctt tca cgt tcc ggt acc ctg 739
 Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser Arg Ser Gly Thr Leu
 200 205 210

gca ggc aga tct tcc aat ctt taggagccct cgccatgtac ctg 783
 Ala Gly Arg Ser Ser Asn Leu
 215 220

<210> 638

<211> 220

<212> PRT

<213> Corynebacterium glutamicum

<400> 38

Val Glu Leu Ala Arg Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly
 1 5 10 15

Thr Gly Lys Leu Thr Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu
 20 25 30

Asp Pro Ser Met Asp Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala

35	40	45
Val Pro Cys Trp Gln Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn 50 55 60		
Ala Val Asp Leu Ile Thr Cys Ala Gln Thr Trp His Trp Val Asp Val 65 70 75 80		
Thr Ala Ala Ser Ala Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala 85 90 95		
Val Leu Leu Val Trp Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His 100 105 110		
Arg Leu Ser Arg Ile Met His Ala Gly Asp Val Leu Lys Pro Gly Phe 115 120 125		
Thr Pro Glu Thr Ala Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr 130 135 140		
Thr Trp Asn Gln His Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His 145 150 155 160		
Thr Arg Ser Tyr Trp Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val 165 170 175		
Asp Gln Asn Leu Gln Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro 180 185 190		
Asp Asn Pro Val Glu Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser 195 200 205		
Arg Ser Gly Thr Leu Ala Gly Arg Ser Ser Asn Leu 210 215 220		

<210> 639
 <211> 1392
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1369)
 <223> RXA00633

<400> 639
 aaagctgcgg taattaaaaa cacttagcgc caaaaattga acactgttca attaacctat 60
 tacactgcag atatacatcc aaaccaagtg acggaggaaa atg gaa aac ccc agc 115
 Met Glu Asn Pro Ser
 1 5
 ttg cgc gag ctt gat cac cga aac atc tgg cac ccg tat gcc gcg ccg 163
 Leu Arg Glu Leu Asp His Arg Asn Ile Trp His Pro Tyr Ala Ala Pro
 10 15 20
 ggc gtg cgc aat aga ctc gtc acc aaa acc gat gga gtg ttt ttg acg 211
 Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp Gly Val Phe Leu Thr
 25 30 35

Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp Lys Val Ala Gln Leu
 280 285 290
 atc agc acc cca aat ggc gga ggt gcg ctg atg cac ggc ccc act ttt
 1027
 Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met His Gly Pro Thr Phe
 295 300 305
 atg gct aat cct ctg gcc tgt gcg gtt tcg cat gct tca tta gaa atc
 1075
 Met Ala Asn Pro Leu Ala Cys Ala Val Ser His Ala Ser Leu Glu Ile
 310 315 320 325
 att gag acc ggc atg tgg cag aaa cag gta aaa aga atc gaa gcc gaa
 1123
 Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys Arg Ile Glu Ala Glu
 330 335 340
 ctt atc gca ggc ctt tcc cca ctt caa cac ctt cca ggg gtt gcc gat
 1171
 Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu Pro Gly Val Ala Asp
 345 350 355
 gtc cgg gtt ctc ggc gcg att ggt gtc atc gaa atg gaa caa aat gtc
 1219
 Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu Met Glu Gln Asn Val
 360 365 370
 aat gtc gaa gaa gct act cag gct gca tta gat cac ggt gtg tgg atc
 1267
 Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp His Gly Val Trp Ile
 375 380 385
 cgc ccc ttt gga cgc ttg ctc tat gtc atg cct cca tat atc acc acg
 1315
 Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro Pro Tyr Ile Thr Thr
 390 395 400 405
 tca gag cag tgc gca cag atc tgc act gcg ctt cat gct gca gtt aaa
 1363
 Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu His Ala Ala Val Lys
 410 415 420

ggg aaa taaaccatgc catttttatt tgt
 1392
 Gly Lys

<210> 640
 <211> 423
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 640
 Met Glu Asn Pro Ser Leu Arg Glu Leu Asp His Arg Asn Ile Trp His
 1 5 10 15
 Pro Tyr Ala Ala Pro Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp
 20 25 30

Gly Val Phe Leu Thr Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met
 35 40 45
 Ser Ser Trp Trp Ser Ala Ile His Gly His Gly His Pro Arg Leu Lys
 50 55 60
 Ala Ala Ala Gln Lys Gln Ile Asp Thr Met Ser His Val Met Phe Gly
 65 70 75 80
 Gly Leu Thr His Glu Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn
 85 90 95
 Leu Thr Gly Asn Ser Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser
 100 105 110
 Val Ser Val Glu Val Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly
 115 120 125
 Gln Gly His Pro Glu Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr
 130 135 140
 His Gly Asp Thr Phe Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly
 145 150 155 160
 Met His Ser Leu Trp Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro
 165 170 175
 Ala Pro Pro Val Arg Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu
 180 185 190
 Arg Ser Met Glu Leu Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile
 195 200 205
 Glu Pro Ile Val Gln Gly Ala Gly Gly Met Arg Phe His Asp Val Ala
 210 215 220
 Leu Ile Glu Gly Val Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu
 225 230 235 240
 Ile Val Asp Glu Ile Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe
 245 250 255
 Ala Thr Leu Ser Asn Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys
 260 265 270
 Ala Leu Thr Gly Gly Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp
 275 280 285
 Lys Val Ala Gln Leu Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met
 290 295 300
 His Gly Pro Thr Phe Met Ala Asn Pro Leu Ala Cys Ala Val Ser His
 305 310 315 320
 Ala Ser Leu Glu Ile Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys
 325 330 335
 Arg Ile Glu Ala Glu Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu
 340 345 350
 Pro Gly Val Ala Asp Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu

355	360	365
Met Glu Gln Asn Val Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp		
370	375	380
His Gly Val Trp Ile Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro		
385	390	395
Pro Tyr Ile Thr Thr Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu		
	405	410
His Ala Ala Val Lys Gly Lys		
	420	

<210> 641
 <211> 795
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(772)
 <223> RXA00632

<400> 641
 tggacgcttg ctctatgtca tgcctccata taccaccacg tcagagcagt gcgcacagat 60
 ctgcactgcg cttcatgctg cagttaaagg gaaataaacc atg cca ttt tta ttt 115
 Met Pro Phe Leu Phe
 1 5
 gtc agc ggt acc gga act ggg gtt ggg aaa acc ttc tcc aca gcc gtt 163
 Val Ser Gly Thr Gly Thr Gly Val Gly Lys Thr Phe Ser Thr Ala Val
 10 15 20
 ttg gtt cga tac tta gcc gat caa gga cac gat gtt ctg ccc gta aag 211
 Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp Val Leu Pro Val Lys
 25 30 35
 cta gtc caa acc ggt gaa ctt cca ggc gag gga gac atc ttt aac att 259
 Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly Asp Ile Phe Asn Ile
 40 45 50

gaa cgc ttg act gga att gct gga gag gaa ttt gct cgt ttc aaa gac 307
 Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe Ala Arg Phe Lys Asp
 55 60 65
 cct ctt gcg cca aat ctg gca gcc cga cga gag ggg gtc gag cca ata 355
 Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu Gly Val Glu Pro Ile
 70 75 80 85
 cag ttt gat cag att atc tcg tgg ctt cgt ggt ttt gac gac cca gat 403
 Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly Phe Asp Asp Pro Asp
 90 95 100
 cgc atc att gtg gtg gag ggc gct ggt ggc ctg ctg gtc aga tta ggg 451
 Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu Leu Val Arg Leu Gly
 105 110 115
 gaa gat ttc acc ctg gca gat gtt gcc tcc gct ttg aat gca ccc tta 499

Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala Leu Asn Ala Pro Leu
 120 125 130

gtg att gtg aca agc acc gga ttg gga agc ctc aac gct gct gaa tta 547
 Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu Asn Ala Ala Glu Leu
 135 140 145

agc gtt gag gca gca aac cgc cga gga ctc aca gtg ttg gga gtc ctc 595
 Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr Val Leu Gly Val Leu
 150 155 160 165

ggc ggt tcg atc cct caa aat cct gat cta gct acg atg ctt aat ctc 643
 Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala Thr Met Leu Asn Leu
 170 175 180

gaa gaa ttt gag aga gtc acc ggc gtg ccc ttt tgg gga gct ttg ccg 691
 Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe Trp Gly Ala Leu Pro
 185 190 195

gaa ggg ttg tca cgg gtg gag ggg ttc gtc gaa aag caa tct ttt ccg 739
 Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu Lys Gln Ser Phe Pro
 200 205 210

gcc ctt gat gcc ttt aag aaa ccg ccg gca agg tgatcgtgaa caccgtgcct 792
 Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg
 215 220

tcg 795

<210> 642
 <211> 224
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 642
 Met Pro Phe Leu Phe Val Ser Gly Thr Gly Thr Gly Val Gly Lys Thr
 1 5 10 15

Phe Ser Thr Ala Val Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp
 20 25 30

Val Leu Pro Val Lys Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly
 35 40 45

Asp Ile Phe Asn Ile Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe
 50 55 60

Ala Arg Phe Lys Asp Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu
 65 70 75 80

Gly Val Glu Pro Ile Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly
 85 90 95

Phe Asp Asp Pro Asp Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu
 100 105 110

Leu Val Arg Leu Gly Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala
 115 120 125

Leu Asn Ala Pro Leu Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu

130	135	140
Asn Ala Ala Glu Leu Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr		
145	150	155 160
Val Leu Gly Val Leu Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala		
	165	170 175
Thr Met Leu Asn Leu Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe		
	180	185 190
Trp Gly Ala Leu Pro Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu		
	195	200 205
Lys Gln Ser Phe Pro Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg		
210	215	220

<210> 643
 <211> 1125
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1102)
 <223> RXA00295

<400> 643
 gtttaaggca cgtgtcattt tgcattgcgcg tgcccaattc ttcttaagtg tgctcaattt 60

ttaagcgcgc agttattgac aaccagcctc taggagatcc atg acc atc ccc ggc 115
 Met Thr Ile Pro Gly
 1 5

acc atc ctt gac acc gcc cgc acc caa gtt ctg gaa cag gga att ggc 163
 Thr Ile Leu Asp Thr Ala Arg Thr Gln Val Leu Glu Gln Gly Ile Gly
 10 15 20

atc cca gac ttg atg gaa tta gcc cac cag gtt cgg ttg aag tgg tgt 259
 Ile Pro Asp Leu Met Glu Leu Ala His Gln Val Arg Leu Lys Trp Cys
 40 45 50

ggg gaa gaa atc gag gtc gag gcc att att tcc ctc aaa act ggc ggt 307
 Gly Glu Glu Ile Glu Val Glu Gly Ile Ile Ser Leu Lys Thr Gly Gly
 55 60 65

tgc cct gaa gat tgt cat ttc tgc tca cag tct ggg ttg ttt gaa tcg 355
 Cys Pro Glu Asp Cys His Phe Cys Ser Gln Ser Gly Leu Phe Glu Ser
 70 75 80 85

ccg gtg cgt tcg gtg tgg ctg gat att ccg aat ctg gtt gaa gcc gct 403
 Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn Leu Val Glu Ala Ala
 90 95 100

```

aaa cag acc gca aaa act ggc gct acc gaa ttc tgt atc gtc gcc gca 451
Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe Cys Ile Val Ala Ala
105 110 115

gtc aag ggg cct gat gag agg ctc atg acc cag ctg gag gaa gca gtc 499
Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln Leu Glu Glu Ala Val
120 125 130

ctc gcg att cac tct gaa gtt gaa att gaa gtc gca gca tcg atc gga 547
Leu Ala Ile His Ser Glu Val Glu Ile Glu Val Ala Ala Ser Ile Gly
135 140 145

acg tta aat aag gaa cag gtg gat cgc ctc gct gct gcc ggc gtg cac 595
Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala Ala Gly Val His
150 155 160 165

cgc tac aac cat aat ttg gaa act gcg cgt tcc tat ttc cct gaa gtt 643
Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser Tyr Phe Pro Glu Val
170 175 180

gtc acc act cat aca tgg gaa gag cgc cgc gaa act ttg cgc ctg gtg 691
Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu Thr Leu Arg Leu Val
185 190 195

gca gaa gct gga atg gaa gtc tgt tcc ggc gga atc tta gga atg ggc 739
Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly Ile Leu Gly Met Gly
200 205 210

gaa act tta gag cag cgc gcc gag ttt gcc gtg cag ctg gcg gag ctt 787
Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val Gln Leu Ala Glu Leu
215 220 225

gat ccg cac gaa gtc ccc atg aac ttc ctt gat cct cgc ccg ggc acc 835
Asp Pro His Glu Val Pro Met Asn Phe Leu Asp Pro Arg Pro Gly Thr
230 235 240 245

cca ttt gcc gat agg gaa ttg atg gac agc cgt gac gct ctg cgc tct 883
Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg Asp Ala Leu Arg Ser
250 255 260

att ggt gcg ttc cgc ctt gcg atg cct cac acc atg ctt cgt ttt gct 931
Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr Met Leu Arg Phe Ala
265 270 275

ggc ggt cgc gag ctg act ttg ggc gac aag ggt tcc gag caa gcc ctc 979
Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly Ser Glu Gln Ala Leu
280 285 290

ctg gga ggc atc aat gcg atg atc gtc gga aac tac ctg act acg ctc
1027
Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn Tyr Leu Thr Thr Leu
295 300 305

ggc cgc cca atg gaa gat gac ctc gac atg atg gat cgt ctc cag ctg
1075
Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met Asp Arg Leu Gln Leu
310 315 320 325

ccc atc aaa gtc ctt aat aag gtc atc taagaagcac gcgcatgaac
1122

```

Pro Ile Lys Val Leu Asn Lys Val Ile
330

gac
1125

<210> 644
<211> 334
<212> PRT
<213> Corynebacterium glutamicum

<400> 644
Met Thr Ile Pro Gly Thr Ile Leu Asp Thr Ala Arg Thr Gln Val Leu
1 5 10 15
Glu Gln Gly Ile Gly Leu Asn Gln Gln Gln Leu Met Glu Val Leu Thr
20 25 30
Leu Pro Glu Glu Gln Ile Pro Asp Leu Met Glu Leu Ala His Gln Val
35 40 45
Arg Leu Lys Trp Cys Gly Glu Glu Ile Glu Val Glu Gly Ile Ile Ser
50 55 60
Leu Lys Thr Gly Gly Cys Pro Glu Asp Cys His Phe Cys Ser Gln Ser
65 70 75 80
Gly Leu Phe Glu Ser Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn
85 90 95
Leu Val Glu Ala Ala Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe
100 105 110
Cys Ile Val Ala Ala Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln
115 120 125
Leu Glu Glu Ala Val Leu Ala Ile His Ser Glu Val Glu Ile Glu Val
130 135 140
Ala Ala Ser Ile Gly Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala
145 150 155 160

Ala Ala Gly Val His Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser
165 170 175
Tyr Phe Pro Glu Val Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu
180 185 190
Thr Leu Arg Leu Val Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly
195 200 205
Ile Leu Gly Met Gly Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val
210 215 220
Gln Leu Ala Glu Leu Asp Pro His Glu Val Pro Met Asn Phe Leu Asp
225 230 235 240
Pro Arg Pro Gly Thr Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg
245 250 255

Asp Ala Leu Arg Ser Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr
260 265 270

Met Leu Arg Phe Ala Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly
275 280 285

Ser Glu Gln Ala Leu Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn
290 295 300

Tyr Leu Thr Thr Leu Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met
305 310 315 320

Asp Arg Leu Gln Leu Pro Ile Lys Val Leu Asn Lys Val Ile
325 330

<210> 645

<211> 1212

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1189)

<223> RXA00223

<400> 645

gcgacctctt tgacatcgcc cctgcgctca tcgaagagat caacaagcgc aagtaggagt 60

tttgaacact ttttatctgg accatgcagc caccacacca atg cgt gag gtg gcc 115
Met Arg Glu Val Ala
1 5

gca gct gcg tgg atg gaa aac gcg cag gca ttg aat ccc gcg agt cag 163
Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu Asn Pro Ala Ser Gln
10 15 20

tac ggt tcg ggg cgt aag gcg cgc agc gtt gcg gat tcg gct cgt gaa 211
Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala Asp Ser Ala Arg Glu
25 30 35

gaa att gct tct ttg ctg ggc tgt gaa cct atc gag gtt gtg ttt acc 259
Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile Glu Val Val Phe Thr
40 45 50

gcg tcc ggc acg gag gca gat aac ctc gct gtg cag ggg tta ttc cac 307
Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val Gln Gly Leu Phe His
55 60 65

gca tcg cct ctc aat cgg att att tct acg ccg atc gag cac ccc ggg 355
Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro Ile Glu His Pro Gly
70 75 80 85

att ctg gaa acc gtc aag gct cta gaa ctt ggc ggg gca gag gcg gag 403
Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly Gly Ala Glu Ala Glu
90 95 100

ctc atg ccg atc ggt cca gat gga cga gtg tct tcc ttc gaa gcg ctg 451
Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser Ser Phe Glu Ala Leu
105 110 115

gac aag cct gcc gcg gtt gcc act atg atg tgg gcg aac aat gag acc	499
Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp Ala Asn Asn Glu Thr	
120 125 130	
ggc gcg att cag ccg gtt tct gag ttc atc gcc gcc gcg cag gcg tcc	547
Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala Ala Ala Gln Ala Ser	
135 140 145	
ggc acg cca aca cac atc gat gcg gtt cag gtc gtt ggc cat ctg ccg	595
Gly Thr Pro Thr His Ile Asp Ala Val Gln Val Val Gly His Leu Pro	
150 155 160 165	
gtc aat ttt gat gag ctc ggc gcc acc act ttg gct gcc tcc gcg cac	643
Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu Ala Ala Ser Ala His	
170 175 180	
aaa ttc ggt gga cca cgt ggc gtc ggc ctg ctg ttg gtg agg cgc tca	691
Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu Leu Val Arg Arg Ser	
185 190 195	
cca gca cct tca gcc gta ttg cac gga ggt ggt cag gag cgc ggc atc	739
Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly Gln Glu Arg Gly Ile	
200 205 210	
cgt cca ggc acc ctt gat gtc gcc ggc gca gct gcc acc gca gcc gca	787
Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala Ala Thr Ala Ala Ala	
215 220 225	
tta cgc gaa gca gtg gcc gag ctt gac ggc gaa gcc acc cgc ctg cgc	835
Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu Ala Thr Arg Leu Arg	
230 235 240 245	
gga ctt aaa aag atg ctt ctc gac gcc atc ctc cac acc atc ccc aac	883
Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu His Thr Ile Pro Asn	
250 255 260	
gta ctg gtc cac acc acc gaa cca tcc ctg cca gga cac ctg cat ctc	931
Val Leu Val His Thr Thr Glu Pro Ser Leu Pro Gly His Leu His Leu	
265 270 275	
tcc ttc cca gga gca gaa ggc gat agt ttg atc atg ctg ctc gac tcc	979
Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile Met Leu Leu Asp Ser	
280 285 290	
ttg cgg atc gaa gcc tcc aca ggt tcg gcc tgc tcc aac ggt gta aac	1027
Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys Ser Asn Gly Val Asn	
295 300 305	
cgt gcc agc cac gtc ctt ttg gcc atg gga att tcc gaa acc gac gcc	1075
Arg Ala Ser His Val Leu Leu Ala Met Gly Ile Ser Glu Thr Asp Ala	
310 315 320 325	
cgt ggt gcc atc cga ttc acc ctc gga aga acc acc act gaa gaa tcc	1123
Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr Thr Thr Glu Glu Ser	
330 335 340	
atc aag gca gtg atc gcc gtg atc gaa gac gta gtg acc agg gct cgt	1171

Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val Val Thr Arg Ala Arg
 345 350 355

act gcg gga atg gct ttt tagcgaccgt aaatcgcata gtg
 1212

Thr Ala Gly Met Ala Phe
 360

<210> 646

<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 646

Met Arg Glu Val Ala Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu
 1 5 10 15

Asn Pro Ala Ser Gln Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala
 20 25 30

Asp Ser Ala Arg Glu Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile
 35 40 45

Glu Val Val Phe Thr Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val
 50 55 60

Gln Gly Leu Phe His Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro
 65 70 75 80

Ile Glu His Pro Gly Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly
 85 90 95

Gly Ala Glu Ala Glu Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser
 100 105 110

Ser Phe Glu Ala Leu Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp
 115 120 125

Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala
 130 135 140

Ala Ala Gln Ala Ser Gly Thr Pro Thr His Ile Asp Ala Val Gln Val
 145 150 155 160

Val Gly His Leu Pro Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu
 165 170 175

Ala Ala Ser Ala His Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu
 180 185 190

Leu Val Arg Arg Ser Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly
 195 200 205

Gln Glu Arg Gly Ile Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala
 210 215 220

Ala Thr Ala Ala Ala Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu
 225 230 235 240

Ala Thr Arg Leu Arg Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu

	245		250		255
His Thr Ile Pro Asn Val Leu Val His Thr Thr Glu Pro Ser Leu Pro					
	260		265		270
Gly His Leu His Leu Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile					
	275		280		285
Met Leu Leu Asp Ser Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys					
	290		295		300
Ser Asn Gly Val Asn Arg Ala Ser His Val Leu Leu Ala Met Gly Ile					
305		310		315	320
Ser Glu Thr Asp Ala Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr					
	325		330		335
Thr Thr Glu Glu Ser Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val					
	340		345		350
Val Thr Arg Ala Arg Thr Ala Gly Met Ala Phe					
	355		360		

<210> 647

<211> 1197

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1174)

<223> RXN00262

<400> 647

acaccgcggg aaagattgca tcaaccgggtg tcgacgtcat ttccggttgga gcgcttaccc 60

attctgtgca tgcacttgac ctaggactcg atattttcta atg ctc tac ctt gat	115
Met Leu Tyr Leu Asp	
1 5	

aat gca gcc acc acc agt gtg cgc aat gaa gca ctt gag gcc atg tgg 163

Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala Leu Glu Ala Met Trp	
10 15 20	

cct tat ctc acc gga gcg ttt ggc aat ccg tca agt ccc cat gag gtg	211
Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser Ser Pro His Glu Val	
25 30 35	

gga aga ctc gcc tct gcg ggg ctg gag gat gct cga act cgg gtg gcc	259
Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala Arg Thr Arg Val Ala	
40 45 50	

cgc att atc gga gga cgc ccc aca cag gtg acg ttt acg tcg ggt gga	307
Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr Phe Thr Ser Gly Gly	
55 60 65	

tca gaa gcc aac aac ctc gct atc aaa gga gcg tgc tta gct aat cct	355
Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala Cys Leu Ala Asn Pro	
70 75 80 85	

cgt ggc cgg cac ctc atc acc acc ccg atc gag cat gac agt gtc cta 403
 Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu His Asp Ser Val Leu
 90 95 100

gaa act gct gct tat ctt gaa agg ttt cat gat ttc gag atc acc tac 451
 Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr
 105 110 115

cta tcc ccc gat cac act ggg ctg atc tcc ccg gag ggt ctc cgc aaa 499
 Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys
 120 125 130

gca gtc agg ccg gac acc aca ttg atc agc att ggt tat gcc aac aat 547
 Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn
 135 140 145

gag gtg gga acc att cag ccg ata gct gag ttg gcg gcg gta agc agt 595
 Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser
 150 155 160 165

acg cct ttt cac acc gat gca gtg caa gct gca cat tta acc ttt gac 643
 Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp
 170 175 180

ttg gga gtt gac gcg tta agt ttg tcg ggt cat aaa ttc ggt gcg cct 691
 Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro
 185 190 195

aaa ggg att gga gtg tta tgg tca aag ctt ccc ctg gag ccg gta atc 739
 Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile
 200 205 210

cat ggc ggc ggc cag gaa aaa ggg ccg cgt agt ggc acg gaa aac gtt 787
 His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val
 215 220 225

gcg ggg gct atc gcc ttt gcc act gcc ttg gaa ttg gcc agg gcg gaa 835
 Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu
 230 235 240 245

tcc tat cca gat ctt ggc gaa ttc atc gag gaa gtt ctc act atc ccg 883
 Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro
 250 255 260

gga gca cac ctg act gga cat cct agg atg cgc att gat gga cac gca 931
 Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala
 265 270 275

tct ttt ctc ttc gac agc ata gga tct gaa act gtt ctt ctg gaa ttg 979
 Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu
 280 285 290

gaa cgc caa ggc att gtg tgc tcc cct ggt tct gcc tgt ggt tcc gga
 1027
 Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly
 295 300 305

gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt gag gag gat caa gca
 1075
 Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala
 310 315 320 325

cga acg gct gtg cgc tgt act ttt agt aca aca cac agc cgt gaa gat
1123

Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp
330 335 340

gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg gtc gcc tta atc aga
1171

Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg
345 350 355

ggg tgacgctagt cagaggttta cgg

1197

Gly

<210> 648

<211> 358

<212> PRT

<213> Corynebacterium glutamicum

<400> 648

Met Leu Tyr Leu Asp Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala
1 5 10 15

Leu Glu Ala Met Trp Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser
20 25 30

Ser Pro His Glu Val Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala
35 40 45

Arg Thr Arg Val Ala Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr
50 55 60

Phe Thr Ser Gly Gly Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala
65 70 75 80

Cys Leu Ala Asn Pro Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu
85 90 95

His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp
100 105 110

Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro
115 120 125

Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile
130 135 140

Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu
145 150 155 160

Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala
165 170 175

His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His
180 185 190

Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro
195 200 205

Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser
210 215 220

Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu
225 230 235 240

Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu
245 250 255

Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg
260 265 270

Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr
275 280 285

Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser
290 295 300

Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu
305 310 315 320

Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr
325 330 335

His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala
340 345 350

Val Ala Leu Ile Arg Gly
355

<210> 649

<211> 920

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (79)..(897)

<223> FRXA00262

<400> 649

cacacaggtg acgtttacgt cgggtggatc agaagccaac aacctcgctt atcaaaggag 60

cgtgcttagc taatcctagt gcc ggg cac ctc atc acc acc ccg atc gag 111
Val Ala Gly His Leu Ile Thr Thr Pro Ile Glu
1 5 10

cat gac agt gtc cta gaa act gct gct tat ctt gaa agg ttt cat gat 159
His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp
15 20 25

ttc gag atc acc tac cta tcc ccc gat cac act ggg ctg atc tcc ccg 207
Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro
30 35 40

gag ggt ctc cgc aaa gca gtc agg ccg gac acc aca ttg atc agc att 255
Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile
45 50 55

ggt tat gcc aac aat gag gtg gga acc att cag ccg ata gct gag ttg 303
 Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu
 60 65 70 75

gcg gcg gta agc agt acg cct ttt cac acc gat gca gtg caa gct gca 351
 Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala
 80 85 90

cat tta acc ttt gac ttg gga gtt gac gcg tta agt ttg tgg ggt cat 399
 His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His
 95 100 105

aaa ttc ggt gcg cct aaa ggg att gga gtg tta tgg tca aag ctt ccc 447
 Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro
 110 115 120

ctg gag ccg gta atc cat ggc ggc ggc cag gaa aaa ggg cgg cgt agt 495
 Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser
 125 130 135

ggc acg gaa aac gtt gcg ggg gct atc gcc ttt gcc act gcc ttg gaa 543
 Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu
 140 145 150 155

ttg gcc agg gcg gaa tcc tat cca gat ctt ggc gaa ttc atc gag gaa 591
 Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu
 160 165 170

gtt ctc act atc ccg gga gca cac ctg act gga cat cct agg atg cgc 639
 Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg
 175 180 185

att gat gga cac gca tct ttt ctc ttc gac agc ata gga tct gaa act 687
 Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr
 190 195 200

gtt ctt ctg gaa ttg gaa cgc caa ggc att gtg tgc tcc cct ggt tct 735
 Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser
 205 210 215

gcc tgt ggt tcc gga gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt 783
 Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu
 220 225 230 235

gag gag gat caa gca cga acg gct gtg cgc tgt act ttt agt aca aca 831
 Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr
 240 245 250

cac agc cgt gaa gat gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg 879
 His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala
 255 260 265

gtc gcc tta atc aga ggg tgacgctagt cagaggttta cgg 920
 Val Ala Leu Ile Arg Gly
 270

<210> 650

<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 650

Val Ala Gly His Leu Ile Thr Thr Pro Ile Glu His Asp Ser Val Leu
 1 5 10 15

Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr
 20 25 30

Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys
 35 40 45

Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn
 50 55 60

Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser
 65 70 75 80

Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp
 85 90 95

Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro
 100 105 110

Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile
 115 120 125

His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val
 130 135 140

Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu
 145 150 155 160

Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro
 165 170 175

Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala
 180 185 190

Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu
 195 200 205

Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly
 210 215 220

Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala
 225 230 235 240

Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp
 245 250 255

Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg
 260 265 270

Gly

<210> 651

<211> 1296

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1273)

<223> RXN00435

<400> 651

```

cgacaggtga attcatgcac gtttgagtgt cccgtgtgtg gggtaatgtt gtccaagaga 60

gtggaaggaa atgctgtggc ggttgaaagg agtgcctttc gtg ggt ttt gat gtg 115
                               Val Gly Phe Asp Val
                               1                               5

gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac 163
Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr
                               10                               15                               20

ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga 211
Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly
                               25                               30                               35

gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg 259
Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser
                               40                               45                               50

cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg 307
Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala
                               55                               60                               65

tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg 355
Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg
70                               75                               80                               85

cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt 403
Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg
90                               95                               100

cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc 451
Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr
105                               110                               115

gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat 499
Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp
120                               125                               130

ttg ggc acc ggc atg ctg ccg gat tgg cag tac gag aag ctt gtt gac 547
Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Glu Lys Leu Val Asp
135                               140                               145

ggc tcg acg cgc ctt gtc gtg ctc agc gcc gcg cac ccg ctg ctc ggc 595
Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala His Pro Leu Leu Gly
150                               155                               160                               165

acg gtc gcc cca gtg ggc aag att gtg gat aaa gtg cgg gcg cgt tcg 643
Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys Val Arg Ala Arg Ser
170                               175                               180

cgt gcc tgg gtg ctt gtc gac gcc acc acc tac gca gcc tac cgc ccc 691
Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro
185                               190                               195

```

ctg cgc cta gac gag tgg gaa gcc gat atc gtc atg ctt gat ctc ggc 739
 Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly
 200 205 210

gag ttg ggc ggc ccg cag att tcg gcg ttg att ttc cgt gat acc tcg 787
 Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser
 215 220 225

atg ttc ccg cgc ctg gat cgc acc gtt cca ctc gaa ctg ccc gca agc 835
 Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser
 230 235 240 245

tcc ctg ccg cat ggg ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac 883
 Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro Asn Leu Val Arg His
 250 255 260

ctg gga aac ctg gat gaa aac gcc ccg tcc gtc gtt gag gcg atg ggg 931
 Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly
 265 270 275

gag atg gcg aaa ttc cac aag gga ctt ttt gag cat ctt gtg gaa tcg 979
 Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu His Leu Val Glu Ser
 280 285 290

ctc gaa gga ctt cac gcg gtg cat atc gtg gga att tcc ggc gat gcc
 1027
 Leu Glu Gly Leu His Ala Val His Ile Val Gly Ile Ser Gly Asp Ala
 295 300 305

gca ggt caa gac gcc ccg ttc ctg gat cga gtg ccc cgc ttg acc ttc
 1075
 Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe
 310 315 320 325

acc atg gaa ggc gtg ccc gca gat atg gtg tac cgc cga ttg gtg gac
 1123
 Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp
 330 335 340

aat cgt ttg atc act acc gtc agc cct gct gac ccg ctg ctc gaa gca
 1171
 Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala
 345 350 355

atg ggt gtg act gaa gct ggc gga tcg atc act atc gga cta agc ccg
 1219
 Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro
 360 365 370

ttt agc acc tac tat gaa gtg gat cag ctg acc agg gtg ctg gca tcg
 1267
 Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser
 375 380 385

ctt gcc taaaccgcaa gcacgagctt gcc
 1296
 Leu Ala
 390

<210> 652

<211> 391

<212> PRT

<213> Corynebacterium glutamicum

<400> 652

Val Gly Phe Asp Val Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly
 1 5 10 15

Asp Gly Trp Thr Tyr Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu
 20 25 30

Arg Val Ala Ser Gly Val Ala Ala Phe Arg Thr His Ala Gln Ile
 35 40 45

Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala
 50 55 60

Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val
 65 70 75 80

Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu
 85 90 95

Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp
 100 105 110

Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser
 115 120 125

Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr
 130 135 140

Glu Lys Leu Val Asp Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala
 145 150 155 160

His Pro Leu Leu Gly Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys
 165 170 175

Val Arg Ala Arg Ser Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr
 180 185 190

Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val
 195 200 205

Met Leu Asp Leu Gly Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile
 210 215 220

Phe Arg Asp Thr Ser Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu
 225 230 235 240

Glu Leu Pro Ala Ser Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro
 245 250 255

Asn Leu Val Arg His Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val
 260 265 270

Val Glu Ala Met Gly Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu
 275 280 285

His Leu Val Glu Ser Leu Glu Gly Leu His Ala Val His Ile Val Gly
 290 295 300

Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val
305 310 315 320

Pro Arg Leu Thr Phe Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr
325 330 335

Arg Arg Leu Val Asp Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp
340 345 350

Pro Leu Leu Glu Ala Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr
355 360 365

Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr
370 375 380

Arg Val Leu Ala Ser Leu Ala
385 390

<210> 653

<211> 638

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(615)

<223> FRXA00435

<400> 653

gtc gac gcc acc acc tac gca gcc tac cgc ccc ctg cgc cta gac gag 48
Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu
1 5 10 15

tgg gaa gcc gat atc gtc atg ctt gat ctc ggc gag ttg ggc ggc ccg 96
Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly Glu Leu Gly Gly Pro
20 25 30

cag att tcg gcg ttg att ttc cgt gat acc tcg atg ttc ccg cgc ctg 144
Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser Met Phe Pro Arg Leu
35 40 45

gat cgc acc gtt cca ctc gaa ctg ccc gca agc tcc ctg ccg cat ggg 192
Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser Ser Leu Pro His Gly
50 55 60

ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac ctg gga aac ctg gat 240
Leu Leu Gly Gly Val Pro Asn Leu Val Arg His Leu Gly Asn Leu Asp
65 70 75 80

gaa aac gcc ccg tcc gtc gtt gag gcg atg ggg gag atg gcg aaa ttc 288
Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly Glu Met Ala Lys Phe
85 90 95

cac aag gga ctt ttt gag cat ctt gtg gaa tcg ctc gaa gga ctt cac 336
His Lys Gly Leu Phe Glu His Leu Val Glu Ser Leu Glu Gly Leu His
100 105 110

gcg gtg cat atc gtg gga att tcc ggc gat gcc gca ggt caa gac gcc 384
Ala Val His Ile Val Gly Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala

115	120	125	
ccg ttc ctg gat cga gtg	ccc cgc ttg acc ttc acc	atg gaa ggc gtg	432
Pro Phe Leu Asp Arg Val	Pro Arg Leu Thr Phe Thr	Met Glu Gly Val	
130	135	140	
ccc gca gat atg gtg tac	cgc cga ttg gtg gac	aat cgt ttg atc act	480
Pro Ala Asp Met Val Tyr	Arg Arg Leu Val Asp	Asn Arg Leu Ile Thr	
145	150	155	160
acc gtc agc cct gct gac	ccg ctg ctc gaa gca	atg ggt gtg act gaa	528
Thr Val Ser Pro Ala Asp	Pro Leu Leu Glu Ala	Met Gly Val Thr Glu	
165	170	175	
gct ggc gga tcg atc act	atc gga cta agc ccg	ttt agc acc tac tat	576
Ala Gly Gly Ser Ile Thr	Ile Gly Leu Ser Pro	Phe Ser Thr Tyr Tyr	
180	185	190	
gaa gtg gat cag ctg acc	agg gtg ctg gca tcg	ctt gcc taaaccgcaa	625
Glu Val Asp Gln Leu Thr	Arg Val Leu Ala Ser	Leu Ala	
195	200	205	
gcacgagctt gcc			638

<210> 654

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 654

Val Asp Ala Thr Thr Tyr	Ala Ala Tyr Arg	Pro Leu Arg Leu Asp	Glu
1	5	10	15

Trp Glu Ala Asp Ile Val	Met Leu Asp Leu Gly	Glu Leu Gly Gly	Pro
20	25	30	

Gln Ile Ser Ala Leu Ile	Phe Arg Asp Thr	Ser Met Phe Pro	Arg Leu
35	40	45	

Asp Arg Thr Val Pro Leu	Glu Leu Pro Ala Ser	Ser Leu Pro His	Gly
50	55	60	

Leu Leu Gly Gly Val Pro	Asn Leu Val Arg His	Leu Gly Asn Leu Asp
65	70	80

Glu Asn Ala Pro Ser Val	Val Glu Ala Met Gly	Glu Met Ala Lys Phe
85	90	95

His Lys Gly Leu Phe Glu	His Leu Val Glu Ser	Leu Glu Gly Leu His
100	105	110

Ala Val His Ile Val Gly	Ile Ser Gly Asp Ala	Ala Gly Gln Asp Ala
115	120	125

Pro Phe Leu Asp Arg Val	Pro Arg Leu Thr Phe	Thr Met Glu Gly Val
130	135	140

Pro Ala Asp Met Val Tyr	Arg Arg Leu Val Asp	Asn Arg Leu Ile Thr
145	150	160

Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala Met Gly Val Thr Glu
165 170 175

Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr
180 185 190

Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser Leu Ala
195 200 205

<210> 655

<211> 535

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA02801

<400> 655

cgacaggtga attcatgcac gtttgagtgt cccgtgtgtg gggtaatggt gtccaagaga 60

gtggaaggaa atgctgtggc ggttgaaagg agtgcctttc gtg ggt ttt gat gtg 115
Val Gly Phe Asp Val
1 5

gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac 163
Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr
10 15 20

ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga 211
Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly
25 30 35

gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg 259
Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser
40 45 50

cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg 307
Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala
55 60 65

tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg 355
Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg
70 75 80 85

cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt 403
Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg
90 95 100

cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc 451
Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr
105 110 115

gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat 499
Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp
120 125 130

ttg ggc acc ggc atg ctg ccg gat tgg cag tac cag 535
Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Gln

135

140

145

<210> 656
 <211> 145
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 656
 Val Gly Phe Asp Val Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly
 1 5 10 15
 Asp Gly Trp Thr Tyr Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu
 20 25 30
 Arg Val Ala Ser Gly Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile
 35 40 45
 Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala
 50 55 60
 Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val
 65 70 75 80
 Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu
 85 90 95
 Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp
 100 105 110
 Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser
 115 120 125
 Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr
 130 135 140

Gln
 145

<210> 657
 <211> 1386
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1363)
 <223> RXA02516

<400> 657
 ttcattcacg ttttcgcgaa tggccagatt gtgaccaccg gtggcgctga gcttgctgac 60
 aagctcgagg ctgacggcta cgaccagttc atcaagtaac atg tcc gat ttc ctc 115
 Met Ser Asp Phe Leu
 1 5
 aat gca gat gga tcc ctc aat gtg gat aag gtg cgg gaa gaa ttc cca 163
 Asn Ala Asp Gly Ser Leu Asn Val Asp Lys Val Arg Glu Glu Phe Pro
 10 15 20

atc ctg aag cgc act gtt agg gat ggg aaa ccg ctt gct tac ctg gac 211
 Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro Leu Ala Tyr Leu Asp
 25 30 35

tca ggt gcg aca tcg cag cga ccc gag cgg gtg tgg cgt gca gag gag 259
 Ser Gly Ala Thr Ser Gln Arg Pro Glu Arg Val Trp Arg Ala Glu Glu
 40 45 50

cac ttt gtg ctg cac acc aac gcc ccc gtg cac cgc ggt gcc tac caa 307
 His Phe Val Leu His Thr Asn Ala Pro Val His Arg Gly Ala Tyr Gln
 55 60 65

ctg gct gag gaa gca acg gat gct tat gaa ggt gcc cgc gag aag atc 355
 Leu Ala Glu Glu Ala Thr Asp Ala Tyr Glu Gly Ala Arg Glu Lys Ile
 70 75 80 85

gct gcc ttt gtt ggt gcc gag cag cat gaa att gcg ttc act aag aat 403
 Ala Ala Phe Val Gly Ala Glu Gln His Glu Ile Ala Phe Thr Lys Asn
 90 95 100

gca act gaa gca ctc aat ctt gtt gcg tac acc ttg ggt gat gac cgt 451
 Ala Thr Glu Ala Leu Asn Leu Val Ala Tyr Thr Leu Gly Asp Asp Arg
 105 110 115

tcc ggt aag tat cgt gtc cag gcc ggg gat acc gtg gtc atc acg gag 499
 Ser Gly Lys Tyr Arg Val Gln Ala Gly Asp Thr Val Val Ile Thr Glu
 120 125 130

cta gag cac cac gca aac ttg gtg cca tgg cag gag ctg tgc cgt cga 547
 Leu Glu His His Ala Asn Leu Val Pro Trp Gln Glu Leu Cys Arg Arg
 135 140 145

acc ggt gcg aca ttg aag tgg tac aag gtg act gaa gat ggt cgc att 595
 Thr Gly Ala Thr Leu Lys Trp Tyr Lys Val Thr Glu Asp Gly Arg Ile
 150 155 160 165

gat ctc gat tca ctc gag ctt gat gaa act gtc aag gtc gtt gcc ttc 643
 Asp Leu Asp Ser Leu Glu Leu Asp Glu Thr Val Lys Val Val Ala Phe
 170 175 180

act cac cag tcc aat gtg acc ggt gct gtg gct gat gtt cca gag ttg 691
 Thr His Gln Ser Asn Val Thr Gly Ala Val Ala Asp Val Pro Glu Leu
 185 190 195

gtt cgt cgt gcc aag gct gtc gcc gct ctc acg gtg ctt gat gcg tgc 739
 Val Arg Arg Ala Lys Ala Val Gly Ala Leu Thr Val Leu Asp Ala Cys
 200 205 210

cag tct gtt cct cat atg cca gtg aat ttc cac gag ctg gat gta gat 787
 Gln Ser Val Pro His Met Pro Val Asn Phe His Glu Leu Asp Val Asp
 215 220 225

ttc tct gca ttc tct ggc cat aag atg ctg gga cct gca gcc gtg ggc 835
 Phe Ser Ala Phe Ser Gly His Lys Met Leu Gly Pro Ala Gly Val Gly
 230 235 240 245

gtt gtg tat gca aag tcc cca atc ttg gat gaa ctg cca cca ttt ttg 883
 Val Val Tyr Ala Lys Ser Pro Ile Leu Asp Glu Leu Pro Pro Phe Leu
 250 255 260

act ggt ggt tcc atg att gaa gtt gtc acc atg gag ggt tcc acc tac 931

Thr Gly Gly Ser Met Ile Glu Val Val Thr Met Glu Gly Ser Thr Tyr
 265 270 275

gct gcc gca cct caa cgt ttt gag gcc ggc acg cag atg acc agc cag 979
 Ala Ala Ala Pro Gln Arg Phe Glu Ala Gly Thr Gln Met Thr Ser Gln
 280 285 290

gtt gtg ggc ttg ggt gct gcc gtg gac atg ctg aat gaa atc ggt atg
 1027
 Val Val Gly Leu Gly Ala Ala Val Asp Met Leu Asn Glu Ile Gly Met
 295 300 305

gaa gca atc gca gcg cat gag cac gca ttg act gct tac gcg ttg gaa
 1075
 Glu Ala Ile Ala Ala His Glu His Ala Leu Thr Ala Tyr Ala Leu Glu
 310 315 320 325

aag ctc acg gca att aag gga cta acc att gct ggt cct ttg act gca
 1123
 Lys Leu Thr Ala Ile Lys Gly Leu Thr Ile Ala Gly Pro Leu Thr Ala
 330 335 340

gag cag cgc ggc ggt gca atc agc ttc ggt gtc gag ggc att cac cca
 1171
 Glu Gln Arg Gly Gly Ala Ile Ser Phe Gly Val Glu Gly Ile His Pro
 345 350 355

cac gat cta ggc caa gtg ctt gac gat cag ggc gtg aat atc cgc gtc
 1219
 His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly Val Asn Ile Arg Val
 360 365 370

ggc cac cac tgc gcg tgg ccc gtg cac cgc agc atg aac gta caa tcg
 1267
 Gly His His Cys Ala Trp Pro Val His Arg Ser Met Asn Val Gln Ser
 375 380 385

aca gca aga gca tct ttc tat ctc tat aac acc ttc gaa gaa atc gac
 1315
 Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr Phe Glu Glu Ile Asp
 390 395 400 405

cgc ctc gcg gca gcg atc gag aag gcc aag caa ttc ttt gga gtt gag
 1363
 Arg Leu Ala Ala Ala Ile Glu Lys Ala Lys Gln Phe Phe Gly Val Glu
 410 415 420

taatgaacct tgagcagatg tac
 1386

<210> 658
 <211> 421
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 658
 Met Ser Asp Phe Leu Asn Ala Asp Gly Ser Leu Asn Val Asp Lys Val
 1 5 10 15
 Arg Glu Glu Phe Pro Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro

20					25					30						
Leu	Ala	Tyr	Leu	Asp	Ser	Gly	Ala	Thr	Ser	Gln	Arg	Pro	Glu	Arg	Val	
35					40					45						
Trp	Arg	Ala	Glu	Glu	His	Phe	Val	Leu	His	Thr	Asn	Ala	Pro	Val	His	
50					55					60						
Arg	Gly	Ala	Tyr	Gln	Leu	Ala	Glu	Glu	Ala	Thr	Asp	Ala	Tyr	Glu	Gly	
65					70					75					80	
Ala	Arg	Glu	Lys	Ile	Ala	Ala	Phe	Val	Gly	Ala	Glu	Gln	His	Glu	Ile	
85					90					95						
Ala	Phe	Thr	Lys	Asn	Ala	Thr	Glu	Ala	Leu	Asn	Leu	Val	Ala	Tyr	Thr	
100					105					110						
Leu	Gly	Asp	Asp	Arg	Ser	Gly	Lys	Tyr	Arg	Val	Gln	Ala	Gly	Asp	Thr	
115					120					125						
Val	Val	Ile	Thr	Glu	Leu	Glu	His	His	Ala	Asn	Leu	Val	Pro	Trp	Gln	
130					135					140						
Glu	Leu	Cys	Arg	Arg	Thr	Gly	Ala	Thr	Leu	Lys	Trp	Tyr	Lys	Val	Thr	
145					150					155					160	
Glu	Asp	Gly	Arg	Ile	Asp	Leu	Asp	Ser	Leu	Glu	Leu	Asp	Glu	Thr	Val	
165					170					175						
Lys	Val	Val	Ala	Phe	Thr	His	Gln	Ser	Asn	Val	Thr	Gly	Ala	Val	Ala	
180					185					190						
Asp	Val	Pro	Glu	Leu	Val	Arg	Arg	Ala	Lys	Ala	Val	Gly	Ala	Leu	Thr	
195					200					205						
Val	Leu	Asp	Ala	Cys	Gln	Ser	Val	Pro	His	Met	Pro	Val	Asn	Phe	His	
210					215					220						
Glu	Leu	Asp	Val	Asp	Phe	Ser	Ala	Phe	Ser	Gly	His	Lys	Met	Leu	Gly	
225					230					235					240	
Pro	Ala	Gly	Val	Gly	Val	Val	Tyr	Ala	Lys	Ser	Pro	Ile	Leu	Asp	Glu	
245					250					255						
Leu	Pro	Pro	Phe	Leu	Thr	Gly	Gly	Ser	Met	Ile	Glu	Val	Val	Thr	Met	
260					265					270						
Glu	Gly	Ser	Thr	Tyr	Ala	Ala	Ala	Pro	Gln	Arg	Phe	Glu	Ala	Gly	Thr	
275					280					285						
Gln	Met	Thr	Ser	Gln	Val	Val	Gly	Leu	Gly	Ala	Ala	Val	Asp	Met	Leu	
290					295					300						
Asn	Glu	Ile	Gly	Met	Glu	Ala	Ile	Ala	Ala	His	Glu	His	Ala	Leu	Thr	
305					310					315					320	
Ala	Tyr	Ala	Leu	Glu	Lys	Leu	Thr	Ala	Ile	Lys	Gly	Leu	Thr	Ile	Ala	
325					330					335						
Gly	Pro	Leu	Thr	Ala	Glu	Gln	Arg	Gly	Gly	Ala	Ile	Ser	Phe	Gly	Val	
340					345					350						

Glu Gly Ile His Pro His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly
355 360 365

Val Asn Ile Arg Val Gly His His Cys Ala Trp Pro Val His Arg Ser
370 375 380

Met Asn Val Gln Ser Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr
385 390 395 400

Phe Glu Glu Ile Asp Arg Leu Ala Ala Ala Ile Glu Lys Ala Lys Gln
405 410 415

Phe Phe Gly Val Glu
420

<210> 659

<211> 570

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(547)

<223> RXA02517

<400> 659

cgacagcaag agcatctttc tatctctata acaccttcga agaaatcgac cgcctcgcg 60

cagcgatcga gaaggccaag caattctttg gagttgagta atg aac ctt gag cag 115
Met Asn Leu Glu Gln
1 5

atg tac cag gag gtg atc ctg gac cac tac aaa aac cca cag cac aag 163
Met Tyr Gln Glu Val Ile Leu Asp His Tyr Lys Asn Pro Gln His Lys
10 15 20

ggc ctt cgg gat cct ttc gat gct gag gtt cac cac gtc aac cct tct 211
Gly Leu Arg Asp Pro Phe Asp Ala Glu Val His His Val Asn Pro Ser
25 30 35

~~tgt ggc gac gaa ttg aat ctg tgc gtg aag ctg tct gag gac ggc tcc~~ 259
Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu Ser Glu Asp Gly Ser
40 45 50

acc gtg gag gac gtc tcc tac gaa gca gtt ggt tgc tca atc agc cag 307
Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly Cys Ser Ile Ser Gln
55 60 65

gcc tcc acg tcc gtt atg gcc gag gag atc gtg ggc caa ccc gtc gac 355
Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val Gly Gln Pro Val Asp
70 75 80 85

aag gcg ctg gaa aag ctc aca gaa ttt gag aag atg atc gtt tcc cgc 403
Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys Met Ile Val Ser Arg
90 95 100

ggt cag ttt gtt ggc gat gaa gat ctc atc gga gat ggc gtt gct ttc 451
Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly Asp Gly Val Ala Phe
105 110 115

tcc gga gtc gcc aag tac ccg gca cgc gtg aag tgc gcg ctg ctt ggg 499
 Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys Cys Ala Leu Leu Gly
 120 125 130

tgg aag gct ttc cag gcg gca acc gct gac gct gtt gcg cac gca cat 547
 Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala Val Ala His Ala His
 135 140 145

tagcccgctg tattaattgg agg 570

<210> 660

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 660

Met Asn Leu Glu Gln Met Tyr Gln Glu Val Ile Leu Asp His Tyr Lys
 1 5 10 15

Asn Pro Gln His Lys Gly Leu Arg Asp Pro Phe Asp Ala Glu Val His
 20 25 30

His Val Asn Pro Ser Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu
 35 40 45

Ser Glu Asp Gly Ser Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly
 50 55 60

Cys Ser Ile Ser Gln Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val
 65 70 75 80

Gly Gln Pro Val Asp Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys
 85 90 95

Met Ile Val Ser Arg Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly
 100 105 110

Asp Gly Val Ala Phe Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys
 115 120 125

Cys Ala Leu Leu Gly Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala
 130 135 140

Val Ala His Ala His
 145

<210> 661

<211> 1167

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1144)

<223> RXA01747

<400> 661

cgaagtagag ccgattgcag aatcggcgga atgagacgtc gaaaagcggt taagctttcc 60

ctaaaaatat cactaactcg aaagatgtaa ggttgcat	gtg act atc gca cct	115
	Val Thr Ile Ala Pro	
	1 5	
gaa gga cga cga ctg cta cgc gtc gaa gct cga aac tca gaa acc ccg		163
Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg Asn Ser Glu Thr Pro		
	10 15 20	
att gag acg aag cct cga tgg att aga aac cag gtc aaa aac gga cct		211
Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln Val Lys Asn Gly Pro		
	25 30 35	
gag tat cag gat atg aag gaa cgt gtc gct ggc gca tca cta cac act		259
Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly Ala Ser Leu His Thr		
	40 45 50	
gtg tgt cag gag gct ggc tgt cct aat atc cat gag tgt tgg gaa tcc		307
Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His Glu Cys Trp Glu Ser		
	55 60 65	
cgt gag gca acc ttc ctc att ggt ggc gcc aac tgc tct cgc cgc tgt		355
Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn Cys Ser Arg Arg Cys		
	70 75 80 85	
gat ttc tgc atg atc aac tgc gct cgc cct gag cca ctc gac cgc ggt		403
Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu Pro Leu Asp Arg Gly		
	90 95 100	
gag cca ctg cgt gtc gct gag tct gtt cgt gag atg cag ctg aat tac		451
Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu Met Gln Leu Asn Tyr		
	105 110 115	
tcc acc atc acc ggt gtt acc cgt gat gat ctg gat gat gaa ggc gca		499
Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu Asp Asp Glu Gly Ala		
	120 125 130	
tgg ctg tac tca gaa gtg gtt cgt aag atc cac gag ctg aac cca cac		547
Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His Glu Leu Asn Pro His		
	135 140 145	
acc ggt gtg gaa aac ctg gtg cct gat ttc tcc ggc aag aag gat ctg		595
Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser Gly Lys Lys Asp Leu		
	150 155 160 165	
ctg cag gaa gtt ttt gaa tcc cgc cca gag gtt ttc gct cac aac gtg		643
Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val Phe Ala His Asn Val		
	170 175 180	
gaa act gtg cca cgt att ttc aag cgc att cgc cca gca ttc cgc tac		691
Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg Pro Ala Phe Arg Tyr		
	185 190 195	
gag cgt tca ctt gat gtg atc cgt cag gct cgc gat ttc ggt ctg gtg		739
Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg Asp Phe Gly Leu Val		
	200 205 210	
acc aag tcc aac ctg att ttg ggc atg ggt gaa acc aag gaa gaa atc		787
Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu Thr Lys Glu Glu Ile		
	215 220 225	

acc gag gcg ctg cag gat ctg cac gac gct ggc tgt gac atc atc acc 835
 Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly Cys Asp Ile Ile Thr
 230 235 240 245

atc acc cag tac ctg cgt cct ggt cct ttg ttc cac ccc atc gag cgt 883
 Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe His Pro Ile Glu Arg
 250 255 260

tgg gtg aag cct gag gag ttc ctc gag cac gct gat gct gca aag gaa 931
 Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala Asp Ala Ala Lys Glu
 265 270 275

atg ggc ttc gct gct gtt atg tcc ggc cca ttg gtt cgt tcc tct tac 979
 Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu Val Arg Ser Ser Tyr
 280 285 290

cgt gca ggc cgt ctg tac gcg cag gcc atg gag ttc cgt ggc gag gaa
 1027
 Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu Phe Arg Gly Glu Glu
 295 300 305

atc cca gca cac ctc gcg cac ctg aag gat act tcc gga gga tcc acc
 1075
 Ile Pro Ala His Leu Ala His Leu Lys Asp Thr Ser Gly Gly Ser Thr
 310 315 320 325

gcc cag gaa gca tct aca ctt ctg gag cgt tac ggt gct tcc gaa gac
 1123
 Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr Gly Ala Ser Glu Asp
 330 335 340

acc cca gtg gtg tcc ttc aac taagcccgaa gttttttaac cgc
 1167
 Thr Pro Val Val Ser Phe Asn
 345

<210> 662

<211> 348

<212> PRT

<213> Corynebacterium glutamicum

<400> 662

Val Thr Ile Ala Pro Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg
 1 5 10 15

Asn Ser Glu Thr Pro Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln
 20 25 30

Val Lys Asn Gly Pro Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly
 35 40 45

Ala Ser Leu His Thr Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His
 50 55 60

Glu Cys Trp Glu Ser Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn
 65 70 75 80

Cys Ser Arg Arg Cys Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu
 85 90 95

Pro Leu Asp Arg Gly Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu
 100 105 110
 Met Gln Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu
 115 120 125
 Asp Asp Glu Gly Ala Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His
 130 135 140
 Glu Leu Asn Pro His Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser
 145 150 155 160
 Gly Lys Lys Asp Leu Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val
 165 170 175
 Phe Ala His Asn Val Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg
 180 185 190
 Pro Ala Phe Arg Tyr Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg
 195 200 205
 Asp Phe Gly Leu Val Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu
 210 215 220
 Thr Lys Glu Glu Ile Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly
 225 230 235 240
 Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe
 245 250 255
 His Pro Ile Glu Arg Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala
 260 265 270
 Asp Ala Ala Lys Glu Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu
 275 280 285
 Val Arg Ser Ser Tyr Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu
 290 295 300
 Phe Arg Gly Glu Glu Ile Pro Ala His Leu Ala His Leu Lys Asp Thr
 305 310 315 320

Ser Gly Gly Ser Thr Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr
 325 330 335

Gly Ala Ser Glu Asp Thr Pro Val Val Ser Phe Asn
 340 345

<210> 663

<211> 876

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(853)

<223> RXA01746

<400> 663

aaaccgccac tccccittca ctggggagtg gcggttttgt cgtttcatgc atgcagtgtg 60

tgacttatca accttggttag ggctaggggtg gatatctatc atg act gca cca aga	115
Met Thr Ala Pro Arg	
1 5	
gat cct ttt ttc ccc gca gat ctt tct atc cgc gcg tct gca gag ccc	163
Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg Ala Ser Ala Glu Pro	
10 15 20	
att gaa att cag cgg ttg ggt ttg atc gat tat caa gag gcc tgg gat	211
Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr Gln Glu Ala Trp Asp	
25 30 35	
tat caa gca gag ctt gct acc cgt agg gct aat gat gaa atc cct gat	259
Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn Asp Glu Ile Pro Asp	
40 45 50	
cag ctg ctt att ttg gag cac ccg tcg gtg tat acc gca ggt aag cgc	307
Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg	
55 60 65	
acc cag ccg gaa gat ctt ccc acc aac gga ctg ccg gtg atc aat gct	355
Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu Pro Val Ile Asn Ala	
70 75 80 85	
gat cgt ggt ggt cgc atc acg tgg cat ggt cct ggc caa ttg gtg atc	403
Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro Gly Gln Leu Val Ile	
90 95 100	
tat ccg atc atc aaa tta gcc gat ccg atc gat gtg gtt gat tac gta	451
Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp Val Val Asp Tyr Val	
105 110 115	
aga cgc ctc gag gaa gcg ctc atc caa gtt gtc ggc gat atg ggt gtt	499
Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val Gly Asp Met Gly Val	
120 125 130	
gcc ggc gct ggg cgc att gat ggg cgt tcg ggt gtg tgg gtg cca gct	547
Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala	
135 140 145	
cat gat ggt tgg gtg gac agc aag gtt gcg gcc atc ggc att cga ata	595
His Asp Gly Trp Val Asp Ser Lys Val Ala Ala Ile Gly Ile Arg Ile	
150 155 160 165	
act cgt ggt gtt gca atg cac ggt gtg gcc atc aac tgc aac aac acg	643
Thr Arg Gly Val Ala Met His Gly Val Ala Ile Asn Cys Asn Asn Thr	
170 175 180	
ttg gat ttc tat gag cac atc att ccg tgt ggc att gct gat gca ggc	691
Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly Ile Ala Asp Ala Gly	
185 190 195	
ttg agc aca ctc tcg agg gaa ctg aaa agg gac gtt tca gtt gag gaa	739
Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp Val Ser Val Glu Glu	
200 205 210	
tta gtc gag cca tcg atc cgc gca ttg gat gat gct ttg gct ggt cgg	787
Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp Ala Leu Ala Gly Arg	
215 220 225	

ctg gtt gtt tct gat cat tct ttc ggc agc gcg ccc gac cca act aag 835
 Leu Val Val Ser Asp His Ser Phe Gly Ser Ala Pro Asp Pro Thr Lys
 230 235 240 245

aat ctc cct aaa cgg ggg tagtacgagg aattttgtcg gtg 876
 Asn Leu Pro Lys Arg Gly
 250

<210> 664

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 664

Met Thr Ala Pro Arg Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg
 1 5 10 15

Ala Ser Ala Glu Pro Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr
 20 25 30

Gln Glu Ala Trp Asp Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn
 35 40 45

Asp Glu Ile Pro Asp Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr
 50 55 60

Thr Ala Gly Lys Arg Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu
 65 70 75 80

Pro Val Ile Asn Ala Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro
 85 90 95

Gly Gln Leu Val Ile Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp
 100 105 110

Val Val Asp Tyr Val Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val
 115 120 125

Gly Asp Met Gly Val Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly
 130 135 140

Val Trp Val Pro Ala His Asp Gly Trp Val Asp Ser Lys Val Ala Ala
 145 150 155 160

Ile Gly Ile Arg Ile Thr Arg Gly Val Ala Met His Gly Val Ala Ile
 165 170 175

Asn Cys Asn Asn Thr Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly
 180 185 190

Ile Ala Asp Ala Gly Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp
 195 200 205

Val Ser Val Glu Glu Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp
 210 215 220

Ala Leu Ala Gly Arg Leu Val Val Ser Asp His Ser Phe Gly Ser Ala
 225 230 235 240

Pro Asp Pro Thr Lys Asn Leu Pro Lys Arg Gly

245

250

```
<210> 665
<211> 1179
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1156)
<223> RXA02106
```

<400> 665
ggtcgcgcgct ttgcgacgcc cgcctgcggc gggatgactg tgatggaggg gcgcgtcgac 60

aagcaaaatc tctttagcaa attcggttac tgtggggcgc atg aat aac cat ttt 115
Met Asn Asn His Phe
1 5

gag ctc aaa gta cct ggt gga aag ctt gtc gtc gtt gat gtg acc acc 163
Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val Val Asp Val Thr Thr
10 15 20

gat ctg gat tcc att gct gac gtg aag att tcc ggc gat ttc ttc ctc 211
Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser Gly Asp Phe Phe Leu
25 30 35

gaa ccc gat gag gca ttc ttc gcc ctt ggc cgg gcg ctg cag ggg gcg 259
Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg Ala Leu Gln Gly Ala
40 45 50

tcg gtg ggt gat aac act gat cgt ttg cag gca aag ttg gat gga gcg 307
Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala Lys Leu Asp Ala Ala
55 60 65

ttg gcg gaa tat gat gac gtt gag cta cac ggc ttt agc act gcg gat 355
Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly Phe Ser Thr Ala Asp
70 75 80 85

att gct tta gct gtg cgt cgg gca gtc acc ggc gcg caa gat ttc acc 403
Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly Ala Gln Asp Phe Thr
90 95 100

gat tat gaa tgg gaa atc ctg cac cca ggg gtg ctt cct acc cca ctt 451
Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val Leu Pro Thr Pro Leu
105 110 115

aac gtt gcg ttg gat gag ctc ctt ttg gac caa gtt gcc agt ggt cag 499
Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln Val Ala Ser Gly Gln
120 125 130

cgt ggc ccg acg atg cgc att tgg gat tgg gat gat cgc gcc aca gtg 547
 Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp Asp Arg Ala Thr Val
 135 140 145

atc ggt agt ttc cag tca tat gtc aat gaa atc aac caa gaa ggc gtt 595
Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile Asn Gln Glu Gly Val
150 155 160 165

aat gaa cat ggt gtg acc gtg gta cga cgc atg tct ggt ggc ggt gca 643

```

Asn Glu His Gly Val Thr Val Val Arg Arg Met Ser Gly Gly Gly Ala
      170                      175                      180

atg ttt atg gag ggc ggc aac tgc atc acc tat tcc ctg tat gca ccg      691
Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr Ser Leu Tyr Ala Pro
      185                      190                      195

gaa tct ctc gtt gct ggt ttg agc tat gag cag tcc tat gaa tat ttg      739
Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln Ser Tyr Glu Tyr Leu
      200                      205                      210

gat cgt tgg gtg att gct gcg ctg aag aca cac gat gtt gac gct tgg      787
Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His Asp Val Asp Ala Trp
      215                      220                      225

tac gtg cct atc aat gac atc acc tcc acc ggc gga aaa atc ggt ggc      835
Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly Gly Lys Ile Gly Gly
      230                      235                      240

gct gca cag aaa cgt cgc agt ggc gca gtc ctc cac cac gtg acc atg      883
Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu His His Val Thr Met
      250                      255                      260

tcc tat gac atc gat gcg gac atg atg acc cag gtg ttg cgc att gga      931
Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln Val Leu Arg Ile Gly
      265                      270                      275

aag gtg aag att tcc gac aag ggt ctt cgc agc gca aag aag cgc gtt      979
Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser Ala Lys Lys Arg Val
      280                      285                      290

gat cct ctg cgc cgc caa aca ggt gca tca cgt gag caa atc atc gac
1027
Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg Glu Gln Ile Ile Asp
      295                      300                      305

acc cta aag tcc aca ttc agt gct agg tac ggc gcg caa gaa gta gag
1075
Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly Ala Gln Glu Val Glu
      310                      315                      320

ctc agc gat gaa gat ttc gcg gca ggc cac gac cta gta aaa acc aaa
1123

Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp Leu Val Lys Thr Lys
      330                      335                      340

tac gcc acc gag gag tgg act aag cga gtt caa tagtttctat ggatctgcac
1176
Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln
      345                      350

aag
1179

<210> 666
<211> 352
<212> PRT
<213> Corynebacterium glutamicum

<400> 666

```

Met Asn Asn His Phe Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val
 1 5 10 15
 Val Asp Val Thr Thr Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser
 20 25 30
 Gly Asp Phe Phe Leu Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg
 35 40 45
 Ala Leu Gln Gly Ala Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala
 50 55 60
 Lys Leu Asp Ala Ala Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly
 65 70 75 80
 Phe Ser Thr Ala Asp Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly
 85 90 95
 Ala Gln Asp Phe Thr Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val
 100 105 110
 Leu Pro Thr Pro Leu Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln
 115 120 125
 Val Ala Ser Gly Gln Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp
 130 135 140
 Asp Arg Ala Thr Val Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile
 145 150 155 160
 Asn Gln Glu Gly Val Asn Glu His Gly Val Thr Val Val Arg Arg Met
 165 170 175
 Ser Gly Gly Gly Ala Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr
 180 185 190
 Ser Leu Tyr Ala Pro Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln
 195 200 205
 Ser Tyr Glu Tyr Leu Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His
 210 215 220
 Asp Val Asp Ala Trp Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly
 225 230 235 240
 Gly Lys Ile Gly Gly Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu
 245 250 255
 His His Val Thr Met Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln
 260 265 270
 Val Leu Arg Ile Gly Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser
 275 30 285
 Ala Lys Lys Arg Val Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg
 290 295 300
 Glu Gln Ile Ile Asp Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly
 305 310 315 320
 Ala Gln Glu Val Glu Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp

325

330

335

Leu Val Lys Thr Lys Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln
 340 345 350

<210> 667
 <211> 403
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(403)
 <223> RXS01183

<400> 667
 cttgatatga cccgaacacc acacatcaca aattgaatcg gtatcctttg ggggtattagt 60
 ttccgttttta acgacacgac ttgcgaggag tcttaaaata atg gcg ttc tcc gta 115
 Met Ala Phe Ser Val
 1 5
 gag atg ccc gag ctg ggc gaa tca gta acc gaa ggc acg atc acc cag 163
 Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln
 10 15 20
 tgg ttg aag tct gtt ggt gac act gtt gag gta gat gag ccg ttg ctc 211
 Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu
 25 30 35
 gag gtc tca act gac aag gtc gac acc gag att ccc tct cct gtc gcc 259
 Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala
 40 45 50
 ggt gtc atc cta gag att aag gct gaa gag gat gac acc gtc gac gtc 307
 Gly Val Ile Leu Glu Ile Lys Ala Glu Glu Asp Asp Thr Val Asp Val
 55 60 65
 gga ggt gtc att gaa ata ata ggc gat gat gat gag act cct gcc aac 335
 Gly Gly Val Ile Ala Ile Ile Gly Asp Ala Asp Glu Thr Pro Ala Asn
 70 75 80 85
 gaa gct cct gcc gac gag gca cca gct cct gcc gaa gag gaa gaa cca 403
 Glu Ala Pro Ala Asp Glu Ala Pro Ala Pro Ala Glu Glu Glu Glu Pro
 90 95 100

<210> 668
 <211> 101
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 668
 Met Ala Phe Ser Val Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu
 1 5 10 15
 Gly Thr Ile Thr Gln Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val

20	25	30	
Asp Glu Pro Leu Leu Glu Val	Ser Thr Asp Lys Val	Asp Thr Glu Ile	
35	40	45	
Pro Ser Pro Val Ala Gly Val	Ile Leu Glu Ile Lys Ala	Glu Glu Asp	
50	55	60	
Asp Thr Val Asp Val Gly Gly	Val Ile Ala Ile Ile Gly	Asp Ala Asp	
65	70	75	80
Glu Thr Pro Ala Asn Glu Ala	Pro Ala Asp Glu Ala	Pro Ala Pro Ala	
85	90	95	
Glu Glu Glu Glu Pro			
100			
<210> 669			
<211> 1305			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1282)			
<223> RXS01260			
<400> 669			
ctaaacgtgg gctgcattcc ttccaaagtc tctgatcaaa aacgctgaag ttgcccat			
ctttacccat gagaagaaga ccttcggcat caatggcgaa gtg acc ttc aac tat 115			
Val Thr Phe Asn Tyr 5			
gag gat gct cac aag cgt tcc cgt ggc gtt tcc gac aag atc gtt gga 163			
Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly 20			
ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa att cat ggt 211			
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly 35			
ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag 259			
Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys 50			
gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt 307			
Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly 65			
tcg gta gtc aac acc ctc cgt ggc gtt gac ttc tca gag aac gtt gtg 355			
Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val 85			
tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc 403			
Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val 100			
att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt 451			
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly			

105	110	115	
aac tac ggt gta gat gta acc gtc atc gag ttc atg gat cgt gtg ctt			499
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu			
120	125	130	
cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag			547
Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys			
135	140	145	
aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg			595
Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg			
150	155	160	165
gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac			643
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp			
170	175		180
aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc			691
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe			
185	190		195
cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc			739
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu			
200	205		210
acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc			787
Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val			
215	220		225
gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct			835
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala			
230	235		240
cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt			883
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly			
250	255		260
gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc			931
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr			
265	270		275
115 115 115 115 115 115 115 115 115 115 115 115 115 115 115			975
Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala			
280	285		290
aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc			1027
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe			
295	300		305
tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca			1075
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala			
310	315		320
aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg			1123
Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu			
330	335		340

gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag
1171

Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln
345 350 355

aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac
1219

Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His
360 365 370

cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga
1267

Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly
375 380 385

cac atg atc aac ttc tagaatccac ctcgttggcc ctg
1305

His Met Ile Asn Phe
390

<210> 670

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 670

Val Thr Phe Asn Tyr Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser
1 5 10 15

Asp Lys Ile Val Gly Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile
20 25 30

Ile Glu Ile His Gly Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu
35 40 45

Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys
50 55 60

Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe
65 70 75 80

Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala
85 90 95

Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe
100 105 110

Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe
115 120 125

Met Asp Arg Val Leu Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile
130 135 140

Ala Lys Ala Tyr Lys Lys Met Gly Val Lys Leu Leu Pro Gly His Ala
145 150 155 160

Thr Thr Ala Val Arg Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln
165 170 175

Lys Lys Gly Ser Asp Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met

180										185					190						
Val	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn						
		195					200					205									
Thr	Gly	Val	Lys	Leu	Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr						
	210					215					220										
Met	Arg	Thr	Asn	Val	Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala						
225					230					235					240						
Lys	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala						
				245					250					255							
Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met						
			260					265					270								
Met	Pro	Arg	Ala	Thr	Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr						
		275					280					285									
Thr	Glu	Glu	Gln	Ala	Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val						
	290					295					300										
Ala	Ser	Phe	Pro	Phe	Ser	Ala	Asn	Gly	Lys	Ala	Val	Gly	Leu	Ala	Glu						
305					310					315					320						
Thr	Asp	Gly	Phe	Ala	Lys	Ile	Val	Ala	Asp	Ala	Glu	Phe	Gly	Glu	Leu						
				325					330					335							
Leu	Gly	Ala	His	Leu	Val	Gly	Ala	Asn	Ala	Ser	Glu	Leu	Ile	Asn	Glu						
			340					345					350								
Leu	Val	Leu	Ala	Gln	Asn	Trp	Asp	Leu	Thr	Thr	Glu	Glu	Ile	Ser	Arg						
	355					360						365									
Ser	Val	His	Ile	His	Pro	Thr	Leu	Ser	Glu	Ala	Val	Lys	Glu	Ala	Ala						
	370					375					380										
His	Gly	Ile	Ser	Gly	His	Met	Ile	Asn	Phe												
385					390																

<210> 671

<211> 294

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(271)

<223> RXS01261

<400> 671

gtgggtgttt ttcattttct tccactctaa aattaagtat ggaaaaccaa ccgcacccgg 60

atgcacgaca	atgacccact	aaacacgtat	ccttgaatgc	gtg	act	gaa	cat	tat	115
				Val	Thr	Glu	His	Tyr	
				1				5	

gac	gta	gta	gta	ctc	gga	gcc	ggc	ccc	ggg	ggc	tat	gtc	tcc	gcc	atc	163
Asp	Val	Val	Val	Leu	Gly	Ala	Gly	Pro	Gly	Gly	Tyr	Val	Ser	Ala	Ile	

	10	15	20	
cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac				211
Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr				
	25	30	35	
tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct				259
Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser				
	40	45	50	
gat caa aaa cgc tgaagttgcc cataccttta ccc				294
Asp Gln Lys Arg				
	55			

<210> 672

<211> 57

<212> PRT

<213> Corynebacterium glutamicum

<400> 672

Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly			
1	5	10	15

Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val			
	20	25	30

Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile			
	35	40	45

Pro Ser Lys Val Ser Asp Gln Lys Arg	
	50 55

<210> 673

<211> 1005

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(982)

<223> RXA02717

<400> 673

aggcatgtcc ctaacgaaca tcccagcctc atctcaatgg gcaattagcg acgttttgaa 60

gcgtccttca cccggccgag tacctttttc tgtcgagttt atg cca ccc cgc gac	115
	Met Pro Pro Arg Asp
	1 5

gat gca gct gaa gag cgt ctt tac cgc gca gca gag gtc ttc cat gac	163
Asp Ala Ala Glu Glu Arg Leu Tyr Arg Ala Ala Glu Val Phe His Asp	
	10 15 20

ctc ggt gca tcg ttt gtc tcc gtg act tat ggt gct ggc gga tca acc	211
Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Ser Thr	
	25 30 35

cgt gag aga acc tca cgt att gct cga cga tta gcg aaa caa ccg ttg	259
Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu Ala Lys Gln Pro Leu	

40	45	50	
acc act ctg gtg cac ctg acc ctg gtt aac cac act cgc gaa gag atg			307
Thr Thr Leu Val His Leu Thr Leu Val Asn His Thr Arg Glu Glu Met			
55	60	65	
aag gca att ctt cgg gaa tac cta gag ctg gga tta aca aac ctg ttg			355
Lys Ala Ile Leu Arg Glu Tyr Leu Glu Leu Gly Leu Thr Asn Leu Leu			
70	75	80	85
gcg ctt cga gga gat ccg cct gga gac cca tta ggc gat tgg gtg agc			403
Ala Leu Arg Gly Asp Pro Pro Gly Asp Pro Leu Gly Asp Trp Val Ser			
	90	95	100
acc gat gga gga ctg aac tat gcc tct gag ctg atc gat ctt att aag			451
Thr Asp Gly Gly Leu Asn Tyr Ala Ser Glu Leu Ile Asp Leu Ile Lys			
	105	110	115
tcc act cct gag ttc cgg gaa ttc gac ctg ggt atc gcc tcc ttc ccc			499
Ser Thr Pro Glu Phe Arg Glu Phe Asp Leu Gly Ile Ala Ser Phe Pro			
	120	125	130
gaa ggg cat ttc cgg gcg aaa act cta gaa gaa gac acc aaa tac act			547
Glu Gly His Phe Arg Ala Lys Thr Leu Glu Glu Asp Thr Lys Tyr Thr			
	135	140	145
ctg gcg aag ctg cgt gga ggg gca gag tac tcc atc acg cag atg ttc			595
Leu Ala Lys Leu Arg Gly Gly Ala Glu Tyr Ser Ile Thr Gln Met Phe			
	150	155	160
ttt gat gtg gaa gac tac ctg cga ctt cgt gat cgc ctt gtc gct gca			643
Phe Asp Val Glu Asp Tyr Leu Arg Leu Arg Asp Arg Leu Val Ala Ala			
	170	175	180
gac ccc att cat ggt gcg aag cca atc att cct ggc atc atg ccc att			691
Asp Pro Ile His Gly Ala Lys Pro Ile Ile Pro Gly Ile Met Pro Ile			
	185	190	195
acg agc ctg cgg tct gtg cgt cga cag gtc gaa ctg tct ggt gct caa			739
Thr Ser Leu Arg Ser Val Arg Arg Gln Val Glu Leu Ser Gly Ala Gln			
	200	205	210
ttg cgg agc aaa cta gaa gaa tta ctt gtt cga gct gca aac ggc aat			787
Leu Pro Ser Gln Leu Glu Glu Ser Leu Val Arg Ala Ala Asn Gly Asn			
	215	220	225
gaa gaa gcg aac aaa gac gag atc cgc aag gtg ggc att gaa tat tcc			835
Glu Glu Ala Asn Lys Asp Glu Ile Arg Lys Val Gly Ile Glu Tyr Ser			
	230	235	240
acc aat atg gca gag cga ctg att gcc gaa ggt gcg gaa gat ctg cac			883
Thr Asn Met Ala Glu Arg Leu Ile Ala Glu Gly Ala Glu Asp Leu His			
	250	255	260
ttc atg acg ctt aac ttc acc cgt gca acc caa gaa gtg ttg tac aac			931
Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln Glu Val Leu Tyr Asn			
	265	270	275
ctt ggc atg gcg cct gct tgg gga gca gag cac ggc caa gac gcg gtg			979
Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His Gly Gln Asp Ala Val			
	280	285	290

cgt taagccctct taggaatcat gaa
1005
Arg

<210> 674
<211> 294
<212> PRT
<213> Corynebacterium glutamicum

<400> 674
Met Pro Pro Arg Asp Asp Ala Ala Glu Glu Arg Leu Tyr Arg Ala Ala
1 5 10 15
Glu Val Phe His Asp Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly
20 25 30
Ala Gly Gly Ser Thr Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu
35 40 45
Ala Lys Gln Pro Leu Thr Thr Leu Val His Leu Thr Leu Val Asn His
50 55 60
Thr Arg Glu Glu Met Lys Ala Ile Leu Arg Glu Tyr Leu Glu Leu Gly
65 70 75 80
Leu Thr Asn Leu Leu Ala Leu Arg Gly Asp Pro Pro Gly Asp Pro Leu
85 90 95
Gly Asp Trp Val Ser Thr Asp Gly Gly Leu Asn Tyr Ala Ser Glu Leu
100 105 110
Ile Asp Leu Ile Lys Ser Thr Pro Glu Phe Arg Glu Phe Asp Leu Gly
115 120 125
Ile Ala Ser Phe Pro Glu Gly His Phe Arg Ala Lys Thr Leu Glu Glu
130 135 140
Asp Thr Lys Tyr Thr Leu Ala Lys Leu Arg Gly Gly Ala Glu Tyr Ser
145 150 155 160
Ile Thr Gln Met Phe Phe Asp Val Glu Asp Tyr Leu Arg Leu Arg Asp
165 170 175
Arg Leu Val Ala Ala Asp Pro Ile His Gly Ala Lys Pro Ile Ile Pro
180 185 190
Gly Ile Met Pro Ile Thr Ser Leu Arg Ser Val Arg Arg Gln Val Glu
195 200 205
Leu Ser Gly Ala Gln Leu Pro Ser Gln Leu Glu Glu Ser Leu Val Arg
210 215 220
Ala Ala Asn Gly Asn Glu Glu Ala Asn Lys Asp Glu Ile Arg Lys Val
225 230 235 240
Gly Ile Glu Tyr Ser Thr Asn Met Ala Glu Arg Leu Ile Ala Glu Gly
245 250 255

Ala Glu Asp Leu His Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln
260 265 270

Glu Val Leu Tyr Asn Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His
275 280 285

Gly Gln Asp Ala Val Arg
290

<210> 675

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> RXN02027

<400> 675

tcacgtgctc atcgataggc aaactcatgg aaccaagagt acctgcccc gcaaccccaa 60

tcgtcgtacc cctccgaaaa taacggttat ccttagattt atg agc caa act aag 115
Met Ser Gln Thr Lys
1 5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163
Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu
10 15 20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211
Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr
25 30 35

tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259
Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val
40 45 50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307
Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu
55 60 65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355
Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp
70 75 80 85

tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403
Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly
90 95 100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451
Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe
105 110 115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499
Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile
120 125 130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547
Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly

135 140 145 595
 gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac
 Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp
 150 155 160 165
 gat atc 601
 Asp Ile

<210> 676
 <211> 167
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 676
 Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg
 1 5 10 15
 Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile
 20 25 30
 Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala
 35 40 45
 Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp
 50 55 60
 Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu
 65 70 75 80
 Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val
 85 90 95
 Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro
 100 105 110
 Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys
 115 120 125
 Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg
 130 135 140
 Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn
 145 150 155 160
 Gly Glu Ile Arg Asp Asp Ile
 165

<210> 677
 <211> 595
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(595)
 <223> FRXA02027

<400> 677

```

tcacgtgctc atcgataggc aaactcatgg aaccaagagt acctgcccc gcaaccccaa 60
tcgtcgtagc cctccgaaaa taacggttat ccttagattt atg agc caa act aag 115
                                     Met Ser Gln Thr Lys
                                     1                               5
cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163
Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu
                               10                               15                               20
gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211
Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr
                               25                               30                               35
tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259
Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val
                               40                               45                               50
cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307
Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu
                               55                               60                               65
act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355
Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp
                               70                               75                               80                               85
tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403
Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly
                               90                               95                               100
atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451
Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe
                               105                               110                               115
tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499
Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile
                               120                               125                               130
agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547
Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly
                               135                               140                               145

```

```

gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595
Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp
150                               155                               160                               165

```

<210> 678

<211> 165

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 678

```

Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg
 1                               5                               10                               15
Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile
                20                               25                               30
Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala

```

<400> 679																
tggagctcaa caaggcagcg tacatgtttg agtacagctt cgatgacatc accgtgtccg																60
gctacgatcc acacccattg atccgcggca aggtcgcctg																
Met Ile Gly Ala Ile																115
1 5																
tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc																163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro																
10 15 20																
tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc																211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly																
25 30 35																
cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag																259
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys																
40 45 50																
ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc																307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly																
55 60 65																
gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc																355

Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
 70 75 80 85
 tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
 Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
 90 95 100
 gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
 Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
 105 110 115
 ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
 Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
 120 125 130
 tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
 Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
 135 140 145
 atc aag gtt taaggagcaa acaacatgag caa 579
 Ile Lys Val
 150

<210> 680

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 680

Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp
 1 5 10 15
 Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
 20 25 30
 Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
 35 40 45
 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
 50 55 60
 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
 65 70 75 80
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
 85 90 95
 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
 100 105 110
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
 115 120 125
 Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
 130 135 140
 Lys Phe Gln Arg Tyr Ile Lys Val
 145 150

```
<220>
<221> CDS
<222> (101)..(1021)
<223> RXN01321
```

953

gtg aat ggt tat gat ccg gat gcg att gtt ttg gct cgt ttt atg cag 691
 Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln
 185 190 195

att ttg ccg ccg gat ttg tgt gag atg tgg gct ggt cgt gtg ttg aat 739
 Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn
 200 205 210

att cat cac agt ttc ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat 787
 Ile His His Ser Phe Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His
 215 220 225

cag gcg tat agc cgt ggt gtg aag ttg att ggt gcg acc tgc cat tat 835
 Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr
 230 235 240 245

gcg act ggg gat ctg gat gat ggt ccg atc att gag cag gat gtt att 883
 Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile
 250 255 260

cgt gtg acg cat aag gat acg ccg act gag atg cag cgt ttg ggc cgc 931
 Arg Val Thr His Lys Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg
 265 270 275

gat gcg gag aag cag gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag 979
 Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu
 280 285 290

gac cgg gtg ctg gtt tac ggt aac cgc acg gtt gtc ttt gat
 1021
 Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val Val Phe Asp
 295 300 305

taaggctttt tgcttttcga cgc
 1044

<210> 682

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 682

Met Gln Arg Met Thr Pro Ser Ser Pro Glu Val Arg Asn Arg Pro Ser
 1 5 10 15

Ala Ala Pro Glu Glu Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp
 20 25 30

Ser Thr Gly Ile Val Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly
 35 40 45

Gly Trp Ile Thr Glu Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp
 50 55 60

Phe Phe Thr Arg Gln Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile
 65 70 75 80

Glu Gln Leu Arg Glu Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro
 85 90 95

Arg Ala Lys Trp Ser Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val
 100 105 110
 Leu Leu Val Ser Lys Glu Gly His Cys Leu His Asp Leu Leu Gly Arg
 115 120 125
 Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn
 130 135 140
 His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe
 145 150 155 160
 His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp
 165 170 175
 Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu
 180 185 190
 Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala
 195 200 205
 Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly
 210 215 220
 Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly
 225 230 235 240
 Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile
 245 250 255
 Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met
 260 265 270
 Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu
 275 280 285
 Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val
 290 295 300
 Val Phe Asp
 305

<210> 683
 <211> 582
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (23) .. (559)
 <223> FRXA01321

<400> 683
 cttgcacgat ttgtaggtc gtgtg gct gag aat gat tat ccg atg gaa gtt 52
 Val Ala Glu Asn Asp Tyr Pro Met Glu Val
 1 5 10
 gtt gcg gtt gtg ggt aac cat gag aac ttg cgt tat att gcg gag aac 100
 Val Ala Val Val Gly Asn His Glu Asn Leu Arg Tyr Ile Ala Glu Asn
 15 20 25

cat aat gtt ccg ttt ttc cat gtg ccg ttt cct aag gat gcg gtt ggt 148
 His Asn Val Pro Phe Phe His Val Pro Phe Pro Lys Asp Ala Val Gly
 30 35 40

aag cgg aag gcg ttt gac cag gtc gct gag att gtg aat ggt tat gat 196
 Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile Val Asn Gly Tyr Asp
 45 50 55

ccg gat gcg att gtt ttg gct cgt ttt atg cag att ttg ccg ccg gat 244
 Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln Ile Leu Pro Pro Asp
 60 65 70

ttg tgt gag atg tgg gct ggt cgt gtg ttg aat att cat cac agt ttc 292
 Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn Ile His His Ser Phe
 75 80 85 90

ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat cag gcg tat agc cgt 340
 Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg
 95 100 105

ggt gtg aag ttg att ggt gcg acc tgc cat tat gcg act ggg gat ctg 388
 Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr Ala Thr Gly Asp Leu
 110 115 120

gat gat ggt ccg atc att gag cag gat gtt att cgt gtg acg cat aag 436
 Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile Arg Val Thr His Lys
 125 130 135

gat acg ccg act gag atg cag cgt ttg ggc cgc gat gcg gag aag cag 484
 Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln
 140 145 150

gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag gac cgg gtg ctg gtt 532
 Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu Asp Arg Val Leu Val
 155 160 165 170

tac ggt aac cgc acg gtt gtc ttt gat taaggctttt tgcttttcga 579
 Tyr Gly Asn Arg Thr Val Val Phe Asp
 175

cgc 582

<210> 684

<211> 179

<212> PRT

<213> Corynebacterium glutamicum

<400> 684

Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn
 1 5 10 15

His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe
 20 25 30

His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp
 35 40 45

Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu
 50 55 60

Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala
 65 70 75 80

Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly
 85 90 95

Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly
 100 105 110

Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile
 115 120 125

Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met
 130 135 140

Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu
 145 150 155 160

Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val
 165 170 175

Val Phe Asp

<210> 685
 <211> 975
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(952)
 <223> RXA00461

<400> 685
 tgttgggagg gatgacagga ttgtcgaaga taacgtgaag tgggtgttcc ggcattgtgtt 60

tgattgtaag gccttggaag aggggtggaat aatagcgggc gtg act gca atc aaa 115
 Val Thr Ala Ile Lys
 1 5

ctt gat gga aac tta tac cgc ggg gaa att ttc gcc gac ttg gaa cag 163
 Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe Ala Asp Leu Glu Gln
 10 15 20

cgc gtt gct gcg ttg aag gag aaa ggg att gtg ccg ggg ctt gcc acc 211
 Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val Pro Gly Leu Ala Thr
 25 30 35

gtg ctg gtg ggt gat gac cca gcg agc cac tct tac gtg aag atg aag 259
 Val Leu Val Gly Asp Asp Pro Ala Ser His Ser Tyr Val Lys Met Lys
 40 45 50

cat cgt gac tgt gag cag att ggt gtg aac tcg atc cgt aag gat ctg 307
 His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser Ile Arg Lys Asp Leu
 55 60 65

cct gct gat gtc acg cag gaa gag ctt ttc gct gtc atc gat gaa ctg 355
 Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala Val Ile Asp Glu Leu

70	75	80	85	
aac aac gat gat tct tgc act ggt tac att gtg cag ctt cct ttg cct	403			
Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val Gln Leu Pro Leu Pro				
90 95 100				
aag cac ttg gac gaa aac gct gtg ctg gag cgc att gat cca gct aag	451			
Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg Ile Asp Pro Ala Lys				
105 110 115				
gat gct gat ggc ctg cac cct gta aac ctg ggc aag ctt gtg ctc aac	499			
Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly Lys Leu Val Leu Asn				
120 125 130				
gag cca gct cca ctg cca tgc acc ccg aat ggt tcc atc agc ttg ttg	547			
Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly Ser Ile Ser Leu Leu				
135 140 145				
cgt cgt ttc ggc gtt gag ctt gat ggc gcg aag gtt gtt gtc att ggc	595			
Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys Val Val Val Ile Gly				
150 155 160 165				
cgt ggc gtc acc gtt ggt cgc cca att ggc ctg atg ctg acc cgc cgt	643			
Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu Met Leu Thr Arg Arg				
170 175 180				
tcc gag aac tcc acg gtt act ttg tgc cac act ggc acg aag gat ctg	691			
Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr Gly Thr Lys Asp Leu				
185 190 195				
gct gcg gag acc cgt gcg gct gac gtc atc att gct gca gct ggt cag	739			
Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile Ala Ala Ala Gly Gln				
200 205 210				
ccg cac atg ctg acc gca gac atg gtc aag cca ggc gca gcg gtg ctc	787			
Pro His Met Leu Thr Ala Asp Met Val Lys Pro Gly Ala Ala Val Leu				
215 220 225				
gat gtc ggc gtc tcc cgc aag gac ggc aag ttg ctt ggc gac gtc cac	835			
Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu Leu Gly Asp Val His				
230 235 240 245				
aaa gag gtg tgg gaa gta gaa ggc gcg gtc tca cca aac cca ggc ggc	883			
Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser Pro Asn Pro Gly Gly				
250 255 260				
gtt ggc cct ctg acc cgt gca ttc ttg gtg cac aat gtt gtc gag cgc	931			
Val Gly Pro Leu Thr Arg Ala Phe Leu Val His Asn Val Val Glu Arg				
265 270 275				
gct gaa aag ctg gct gga ctc taaaaacaca tgactaatcc cgg	975			
Ala Glu Lys Leu Ala Gly Leu				
280				

<210> 686

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 686

Val Thr Ala Ile Lys Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe
 1 5 10 15
 Ala Asp Leu Glu Gln Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val
 20 25 30
 Pro Gly Leu Ala Thr Val Leu Val Gly Asp Asp Pro Ala Ser His Ser
 35 40 45
 Tyr Val Lys Met Lys His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser
 50 55 60
 Ile Arg Lys Asp Leu Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala
 65 70 75 80
 Val Ile Asp Glu Leu Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val
 85 90 95
 Gln Leu Pro Leu Pro Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg
 100 105 110
 Ile Asp Pro Ala Lys Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly
 115 120 125
 Lys Leu Val Leu Asn Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly
 130 135 140
 Ser Ile Ser Leu Leu Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys
 145 150 155 160
 Val Val Val Ile Gly Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu
 165 170 175
 Met Leu Thr Arg Arg Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr
 180 185 190
 Gly Thr Lys Asp Leu Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile
 195 200 205
 Ala Ala Ala Gly Gln Pro His Met Leu Thr Ala Asp Met Val Lys Pro
 210 215 220
 Gly Ala Ala Val Leu Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu
 225 230 235 240
 Leu Gly Asp Val His Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser
 245 250 255
 Pro Asn Pro Gly Gly Val Gly Pro Leu Thr Arg Ala Phe Leu Val His
 260 265 270
 Asn Val Val Glu Arg Ala Glu Lys Leu Ala Gly Leu
 275 280

<210> 687

<211> 711

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(688)

<223> RXA01514

<400> 687

```

accacagaaa tgccctgtcgt tccagatcag cccatcgatg gtgattccgg gaagtccgct 60
gagggcacac aggagaatcc ggaaaatgaa ggagacaacc gtg gat aac cac gct 115
                                   Val Asp Asn His Ala
                                   1                               5

gca gtt cgc gag ttc gat gag gag cgc gca aca gct gcg att cgt gag 163
Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr Ala Ala Ile Arg Glu
                                   10                               15                               20

ttg ctc atc gct gtg ggt gag gat cca gat cgc gaa ggc ctg ttg gaa 211
Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg Glu Gly Leu Leu Glu
                                   25                               30                               35

acc cca gct cga gtg gct agg gcg tac aag gaa act ttc gcg ggt ctg 259
Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu Thr Phe Ala Gly Leu
                                   40                               45                               50

car gag gat ccc acc act gtg ctg gag aag acg ttc tct gag ggc cat 307
His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr Phe Ser Glu Gly His
                                   55                               60                               65

gaa gag ttg gtt ctg gtt cgt gag atc ccg att tac tcc atg tgt gag 355
Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile Tyr Ser Met Cys Glu
                                   70                               75                               80                               85

cac cac ttg gtg ccg ttc ttt ggc gtg gcg cac att ggt tac att ccg 403
His His Leu Val Pro Phe Phe Gly Val Ala His Ile Gly Tyr Ile Pro
                                   90                               95                               100

ggt aag tcc ggc aag gtg act ggc ctg tcc aag ctg gcg cgt tta gcg 451
Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys Leu Ala Arg Leu Ala
                                   105                               110                               115

gat atg ttt gct aag cga cct cag gtt cag gag cgc ttg acc tcc caa 499
Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu Arg Leu Thr Ser Gln
                                   120                               125                               130

att gcg gat gct ctc gtc gaa aag ctt gat gcc cag gcc gtg gcc gtg 547
Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala Gln Ala Val Ala Val
                                   135                               140                               145

gtg att gaa gct gag cac ctg tgc atg gcc atg cgc gga atc cgt aag 595
Val Ile Glu Ala Glu His Leu Cys Met Ala Met Arg Gly Ile Arg Lys
                                   150                               155                               160                               165

cct ggt gct gtg acc acg acg tct gcg gtg cgc ggc ggt ttt aag aac 643
Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg Gly Gly Phe Lys Asn
                                   170                               175                               180

aac gct gcc tcc cgc gct gag gtg ttc tcc ctg att cgg ggg cac 688
Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu Ile Arg Gly His
                                   185                               190                               195

taaatgaacg tatectcttt gac 711

```

<210> 688

<211> 196

<212> PRT

<213> Corynebacterium glutamicum

<400> 688

Val Asp Asn His Ala Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr
 1 5 10 15

Ala Ala Ile Arg Glu Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg
 20 25 30

Glu Gly Leu Leu Glu Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu
 35 40 45

Thr Phe Ala Gly Leu His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr
 50 55 60

Phe Ser Glu Gly His Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile
 65 70 75 80

Tyr Ser Met Cys Glu His His Leu Val Pro Phe Phe Gly Val Ala His
 85 90 95

Ile Gly Tyr Ile Pro Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys
 100 105 110

Leu Ala Arg Leu Ala Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu
 115 120 125

Arg Leu Thr Ser Gln Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala
 130 135 140

Gln Ala Val Ala Val Val Ile Glu Ala Glu His Leu Cys Met Ala Met
 145 150 155 160

Arg Gly Ile Arg Lys Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg
 165 170 175

Gly Gly Phe Lys Asn Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu
 180 185 190

Ile Arg Gly His
 195

<210> 689

<211> 513

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(490)

<223> RXA01516

<400> 689

tctgcacata tgggagcatg ggggtgtgcgc gtgcacgatg tcccagtatc aagggacgct 60

gttgatgttg ccgcattgtg gcgaagtgga ggaactcacc atg gct gat cgt att 115

											Met	Ala	Asp	Arg	Ile	
											1				5	
gaa	ctt	aaa	ggc	ctt	gaa	tgc	ttc	gga	cac	cac	ggg	gtg	ttc	gac	ttt	163
Glu	Leu	Lys	Gly	Leu	Glu	Cys	Phe	Gly	His	His	Gly	Val	Phe	Asp	Phe	
				10					15					20		
gaa	aaa	gag	caa	ggc	cag	ccc	ttc	att	gtg	gat	gtc	acc	tgc	tgg	atg	211
Glu	Lys	Glu	Gln	Gly	Gln	Pro	Phe	Ile	Val	Asp	Val	Thr	Cys	Trp	Met	
				25					30					35		
gat	ttc	gat	gcc	gca	ggg	gcc	agc	gat	gac	ctt	tcc	gac	acc	gta	gat	259
Asp	Phe	Asp	Ala	Ala	Gly	Ala	Ser	Asp	Asp	Leu	Ser	Asp	Thr	Val	Asp	
				40					45					50		
tac	ggc	gcg	ttg	gca	ttg	ttg	gtt	gct	gaa	atc	gtg	gaa	ggc	cca	tcc	307
Tyr	Gly	Ala	Leu	Ala	Leu	Leu	Val	Ala	Glu	Ile	Val	Glu	Gly	Pro	Ser	
		55					60					65				
agg	gat	ttg	atc	gag	acg	gtg	gcc	acg	gaa	tct	gcg	gat	gct	gtg	atg	355
Arg	Asp	Leu	Ile	Glu	Thr	Val	Ala	Thr	Glu	Ser	Ala	Asp	Ala	Val	Met	
		70					75					80				
gct	aaa	ttt	gat	gcg	ctt	cat	gcg	gtg	gaa	gta	acc	atc	cat	aag	ccc	403
Ala	Lys	Phe	Asp	Ala	Leu	His	Ala	Val	Glu	Val	Thr	Ile	His	Lys	Pro	
				90					95					100		
aaa	gca	ccg	atc	cca	cgt	act	ttt	gct	gac	gtc	gcg	gtg	gtt	gcc	cga	451
Lys	Ala	Pro	Ile	Pro	Arg	Thr	Phe	Ala	Asp	Val	Ala	Val	Val	Ala	Arg	
				105					110					115		
cgt	tcc	agg	aaa	tcc	atg	gct	gct	gga	agg	agc	aac	gcc	taatg	catgc		500
Arg	Ser	Arg	Lys	Ser	Met	Ala	Ala	Gly	Arg	Ser	Asn	Ala				
				120					125					130		
agtttttgtcc atc															513	

<210> 690

<211> 130

<212> PRT

<213> Corynebacterium glutamicum

<400> 690

Met	Ala	Asp	Arg	Ile	Glu	Leu	Lys	Gly	Leu	Glu	Cys	Phe	Gly	His	His
1				5					10					15	
Gly	Val	Phe	Asp	Phe	Glu	Lys	Glu	Gln	Gly	Gln	Pro	Phe	Ile	Val	Asp
			20					25					30		
Val	Thr	Cys	Trp	Met	Asp	Phe	Asp	Ala	Ala	Gly	Ala	Ser	Asp	Asp	Leu
		35					40					45			
Ser	Asp	Thr	Val	Asp	Tyr	Gly	Ala	Leu	Ala	Leu	Leu	Val	Ala	Glu	Ile
	50					55					60				
Val	Glu	Gly	Pro	Ser	Arg	Asp	Leu	Ile	Glu	Thr	Val	Ala	Thr	Glu	Ser
65					70					75					80
Ala	Asp	Ala	Val	Met	Ala	Lys	Phe	Asp	Ala	Leu	His	Ala	Val	Glu	Val
				85					90					95	

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val
 100 105 110

Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser
 115 120 125

Asn Ala
 130

<210> 691

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(952)

<223> RXA01515

<400> 691

taagcctggt gctgtgacca cgacgtctgc ggtgcgcggc ggttttaaga acaacgctgc 60

ctcccgcgct gaggtgttct ccctgattcg ggggcactaa atg aac gta tcc tct 115
 Met Asn Val Ser Ser
 1 5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163
 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr
 10 15 20

gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg 211
 Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala
 25 30 35

atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259
 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp
 40 45 50

gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307
 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser
 55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala
 70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403
 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala
 90 95 100

gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451
 Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu
 105 110 115

gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499
 Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val
 120 125 130

tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547

Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln
 135 140 145
 gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595
 Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp
 150 155 160 165
 gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643
 Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile
 170 175 180
 gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691
 Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp
 185 190 195
 cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739
 Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile
 200 205 210
 ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787
 Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp
 215 220 225
 cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala
 230 235 240 245
 gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His
 250 255 260
 gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931
 Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg
 265 270 275
 agt gga gga act cac cat ggc tgatcgtatt gaacttaaag gcc 975
 Ser Gly Gly Thr His His Gly
 280

<210> 692

<211> 284

<212> PPT

<213> Corynebacterium glutamicum

<400> 692

Met Asn Val Ser Ser Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly
 1 5 10 15
 Ile Val Asn Val Thr Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile
 20 25 30
 Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly
 35 40 45
 Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val
 50 55 60
 Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys
 65 70 75 80

Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala
85 90 95

Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp
100 105 110

Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu
115 120 125

Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly
130 135 140

Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val
145 150 155 160

His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val
165 170 175

Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser
180 185 190

Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser
195 200 205

Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala
210 215 220

Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp
225 230 235 240

Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp
245 250 255

Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val
260 265 270

Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly
275 280

<210> 693

<211> 859

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(859)

<223> RXA02024

<400> 693

cactgatgac ctggatcagg ccgtcaaatt catcgctgat gcacacgctg gattggacgt 60

agcgcgtctc cacaattaag cagtggctac attaggtgtt atg agt tct ttg ccg 115
Met Ser Ser Leu Pro
1 5

gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag 163
Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys
10 15 20

ggt gcg aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc	211
Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val	
25 30 35	
att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc	259
Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly	
40 45 50	
ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca	307
Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro	
55 60 65	
atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt	355
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val	
70 75 80 85	
gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca	403
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala	
90 95 100	
acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag	451
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Val Gln	
105 110 115	
gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg	499
Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly	
120 125 130	
gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg	547
Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val	
135 140 145	
gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt	595
Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg	
150 155 160 165	
gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc	643
Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe	
170 175 180	
ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag	691
Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu	
185 190 195	
gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat	739
Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp	
200 205 210	
ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc	787
Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly	
215 220 225	
acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt	835
Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe	
230 235 240 245	
cgc gtg cat gaa gtt gcg gaa acc	859
Arg Val His Glu Val Ala Glu Thr	
250	

<210> 694
 <211> 253
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 694
 Met Ser Ser Leu Pro Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp
 1 5 10 15
 Ser Phe Tyr Asp Lys Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn
 20 25 30
 Arg Ala Ala Glu Val Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly
 35 40 45
 Gly Val Lys Ala Gly Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile
 50 55 60
 Asp Arg Val Val Pro Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp
 65 70 75 80
 Ile Asp Ile Ser Val Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala
 85 90 95
 Val Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp
 100 105 110
 His Glu Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys
 115 120 125
 Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His
 130 135 140
 Phe Asp Asp Ile Val Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala
 145 150 155 160
 Glu Gln Ala Val Arg Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp
 165 170 175
 Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu
 180 185 190
 Arg Arg Ile Asp Glu Val Val Ala Thr Gly Trp Pro Val Leu Met Ala
 195 200 205
 Leu Ser Asn Lys Asp Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp
 210 215 220
 Lys Arg Val Ala Gly Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg
 225 230 235 240
 Gly Val Ala Ala Phe Arg Val His Glu Val Ala Glu Thr
 245 250

<210> 695
 <211> 579
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00106

<400> 695

```

tggagctcaa caaggcagcg tacatgtttg agtacagctt cgatgacatc accgtgtccg 60
gctacgatcc acacccattg atccgcggca aggtcgccgt atg atc ggt gcg att 115
                               Met Ile Gly Ala Ile
                               1                               5

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
                               10                               15                               20

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
                               25                               30                               35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
Gln Pro Val Ile Met Gly Arg Thr Trp Glu Ser Leu Pro Phe Lys
                               40                               45                               50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
                               55                               60                               65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355
Asp Trp Ser Ala Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
70                               75                               80                               85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
                               90                               95                               100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
105                               110                               115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
120                               125                               130

```

```

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
135                               140                               145

```

```

atc aag gtt taaggagcaa acaacatgag caa 579
Ile Lys Val
150

```

<210> 696

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 696

```

Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp
1                               5                               10                               15

```

Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
20 25 30

Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
35 40 45

Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
50 55 60

Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
65 70 75 80

Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
85 90 95

Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
100 105 110

Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
115 120 125

Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
130 135 140

Lys Phe Gln Arg Tyr Ile Lys Val
145 150

<210> 697

<211> 1556

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1533)

<223> RXA00989

<400> 697

gga att ggc cta gtg gct aac aac gac gga atc ttt gat tcc gaa aat 48
Gly Ile Gly Leu Val Ala Asn Asn Asp Gly Ile Phe Asp Ser Glu Asn
1 5 10 15

gat gac atc acc gta ggc gat gtc acg ttg ggc gag act gga ctg tct 96
Asp Asp Ile Thr Val Gly Asp Val Thr Leu Gly Glu Thr Gly Leu Ser
20 25 30

ttg ccc atc gat ctc gcc ggt gag gta gaa gca cct gcc tcc gag gag 144
Leu Pro Ile Asp Leu Ala Gly Glu Val Glu Ala Pro Ala Ser Glu Glu
35 40 45

atc acc caa gaa gat ttg ctg cgc ctt gcc cag gtg gaa gca gag ttg 192
Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu
50 55 60

gat caa cgt tgg ttg gaa acc aaa att gat ccc act ttc cga cgc atg 240
Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met
65 70 75 80

agc tac atg atg gat ctc atg ggc caa cca cag aat tcc ttc cca gca 288
Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala

85										90					95					
att	cac	gtg	gct	ggc	acc	aac	ggt	aag	acc	tcc	acc	acc	cgc	atg	atc	336				
Ile	His	Val	Ala	Gly	Thr	Asn	Gly	Lys	Thr	Ser	Thr	Thr	Arg	Met	Ile					
			100					105					110							
gag	tcg	ttg	ctg	cgc	gca	ttc	cac	cgc	cgc	acc	ggc	cgg	acc	acc	agc	384				
Glu	Ser	Leu	Leu	Arg	Ala	Phe	His	Arg	Arg	Thr	Gly	Arg	Thr	Thr	Ser					
		115					120					125								
ccg	cac	ctg	cag	ctg	gta	acc	gaa	cgc	atc	gcg	att	gat	ggc	aag	ccc	432				
Pro	His	Leu	Gln	Leu	Val	Thr	Glu	Arg	Ile	Ala	Ile	Asp	Gly	Lys	Pro					
		130				135						140								
atc	cac	ccg	cgt	gat	ttc	gtg	cgc	atc	tac	gaa	gag	att	aag	ccc	tac	480				
Ile	His	Pro	Arg	Asp	Phe	Val	Arg	Ile	Tyr	Glu	Glu	Ile	Lys	Pro	Tyr					
145					150					155					160					
atg	gag	atg	acc	gac	gcc	tgg	tca	gag	gcc	gag	ggc	gga	ccg	aag	atg	528				
Met	Glu	Met	Thr	Asp	Ala	Trp	Ser	Glu	Ala	Glu	Gly	Gly	Pro	Lys	Met					
				165				170						175						
agc	aag	ttt	gag	gca	ctc	gtg	gcc	ctc	gct	tac	gca	ggt	ttt	gcc	gac	576				
Ser	Lys	Phe	Glu	Ala	Leu	Val	Ala	Leu	Ala	Tyr	Ala	Gly	Phe	Ala	Asp					
			180					185					190							
gct	cct	gtt	gac	gtc	gcc	gtc	gtt	gag	gtt	ggt	ctt	ggc	gga	cgc	tgg	624				
Ala	Pro	Val	Asp	Val	Ala	Val	Val	Glu	Val	Gly	Leu	Gly	Gly	Arg	Trp					
		195					200					205								
gat	gcc	act	aac	gtg	atc	aac	gca	gct	gtt	tcc	gtg	atc	acc	ccg	gtg	672				
Asp	Ala	Thr	Asn	Val	Ile	Asn	Ala	Ala	Val	Ser	Val	Ile	Thr	Pro	Val					
		210				215						220								
ggc	atg	gac	cac	gtg	gat	cgc	ctg	ggc	aac	acc	att	ggt	gaa	atc	gct	720				
Gly	Met	Asp	His	Val	Asp	Arg	Leu	Gly	Asn	Thr	Ile	Gly	Glu	Ile	Ala					
225					230					235					240					
ggt	gaa	aag	gcc	ggc	atc	atc	aag	gct	cgt	cct	gca	tct	gag	gat	ggc	768				
Gly	Glu	Lys	Ala	Gly	Ile	Ile	Lys	Ala	Arg	Pro	Ala	Ser	Glu	Asp	Gly					
			245					250						255						
agg	gag	cct	gag	ggc	aac	gtt	gtc	atc	gtg	ggc	aag	cag	gag	cca	gaa	816				
Thr	Glu	Pro	Glu	Gly	Asn	Val	Val	Ile	Val	Gly	Lys	Gln	Glu	Pro	Glu					
			260					265					270							
gca	atg	aac	gtg	att	ctg	cag	caa	gcc	gtg	gac	gtg	gac	gca	gct	gtt	864				
Ala	Met	Asn	Val	Ile	Leu	Gln	Gln	Ala	Val	Asp	Val	Asp	Ala	Ala	Val					
			275					280					285							
gct	cgt	ttg	aac	atg	gaa	ttc	ggc	gtg	gtg	gaa	tcc	gcc	att	gcc	gtt	912				
Ala	Arg	Leu	Asn	Met	Glu	Phe	Gly	Val	Val	Glu	Ser	Ala	Ile	Ala	Val					
		290				295						300								
ggt	gga	cag	cag	ctc	acc	ctg	aag	ggt	ttg	ggc	ggc	gaa	tac	acc	gac	960				
Gly	Gly	Gln	Gln	Leu	Thr	Leu	Lys	Gly	Leu	Gly	Gly	Glu	Tyr	Thr	Asp					
305					310					315					320					
atc	ttc	ctc	cca	ctg	tct	ggc	gcg	cac	caa	gca	gat	aat	gcc	gcg	gtt					
1008																				
Ile	Phe	Leu	Pro	Leu	Ser	Gly	Ala	His	Gln	Ala	Asp	Asn	Ala	Ala	Val					

325 330 335
 gct ctc gca gca gtg gaa gca ttt ttc ggt gca tcc gcc gga cgc cca
 1056
 Ala Leu Ala Ala Val Glu Ala Phe Phe Gly Ala Ser Ala Gly Arg Pro
 340 345 350
 ttg gat atc gac acg gtg cgc gaa ggc ttc gca caa gtt cag tcc cca
 1104
 Leu Asp Ile Asp Thr Val Arg Glu Gly Phe Ala Gln Val Gln Ser Pro
 355 360 365
 ggt cgc ctc gag cgc ctg cgc tct gca cca acc gtg ttc atc gac gca
 1152
 Gly Arg Leu Glu Arg Leu Arg Ser Ala Pro Thr Val Phe Ile Asp Ala
 370 375 380
 gct cac aac cca cac ggt gcc gca gca ctt ggt gca gca cta gac cgt
 1200
 Ala His Asn Pro His Gly Ala Ala Ala Leu Gly Ala Ala Leu Asp Arg
 385 390 395 400
 gac ttt gag ttc cgt cgc ctc atc ggt gtc atc gga gtg ctc tgc gac
 1248
 Asp Phe Glu Phe Arg Arg Leu Ile Gly Val Ile Gly Val Leu Cys Asp
 405 410 415
 aag gat gcc cgc ggc atc ttg gaa tca ctt gag cca tac ctg cat gaa
 1296
 Lys Asp Ala Arg Gly Ile Leu Glu Ser Leu Glu Pro Tyr Leu His Glu
 420 425 430
 att gtg tgc acc cag act gcc tca gag cgc gca ttg gac gca tac gat
 1344
 Ile Val Cys Thr Gln Thr Ala Ser Glu Arg Ala Leu Asp Ala Tyr Asp
 435 440 445
 tta gct gaa tat gct cga gag atc tac ggc gat gag cgt gtg cac gtc
 1392
 Leu Ala Glu Tyr Ala Arg Glu Ile Tyr Gly Asp Glu Arg Val His Val
 450 455 460
 caa gaa gat ctt gct ggc gcg gta gaa ctc gct att gaa cta gca gaa
 1440
 Gln Glu Asp Leu Ala Gly Ala Val Glu Leu Ala Ile Glu Leu Ala Glu
 465 470 475 480
 gac acc gat gta cag tcc gga tca ggt gtt gtg atc acc ggt tca atc
 1488
 Asp Thr Asp Val Gln Ser Gly Ser Gly Val Val Ile Thr Gly Ser Ile
 485 490 495
 gtg acc gcc ggc gat gcg cgc acg ctg ttt gga aag gaa cct gca
 1533
 Val Thr Ala Gly Asp Ala Arg Thr Leu Phe Gly Lys Glu Pro Ala
 500 505 510
 tgagcaagcg tgaagaatca att
 1556

<210> 698

<211> 511

<212> PRT

<213> Corynebacterium glutamicum

<400> 698

Gly Ile Gly Leu Val Ala Asn Asn Asp Gly Ile Phe Asp Ser Glu Asn
 1 5 10 15

Asp Asp Ile Thr Val Gly Asp Val Thr Leu Gly Glu Thr Gly Leu Ser
 20 25 30

Leu Pro Ile Asp Leu Ala Gly Glu Val Glu Ala Pro Ala Ser Glu Glu
 35 40 45

Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu
 50 55 60

Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met
 65 70 75 80

Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala
 85 90 95

Ile His Val Ala Gly Thr Asn Gly Lys Thr Ser Thr Thr Arg Met Ile
 100 105 110

Glu Ser Leu Leu Arg Ala Phe His Arg Arg Thr Gly Arg Thr Thr Ser
 115 120 125

Pro His Leu Gln Leu Val Thr Glu Arg Ile Ala Ile Asp Gly Lys Pro
 130 135 140

Ile His Pro Arg Asp Phe Val Arg Ile Tyr Glu Glu Ile Lys Pro Tyr
 145 150 155 160

Met Glu Met Thr Asp Ala Trp Ser Glu Ala Glu Gly Gly Pro Lys Met
 165 170 175

Ser Lys Phe Glu Ala Leu Val Ala Leu Ala Tyr Ala Gly Phe Ala Asp
 180 185 190

Ala Pro Val Asp Val Ala Val Val Glu Val Gly Leu Gly Gly Arg Trp
 195 200 205

Asp Ala Thr Asn Val Ile Asn Ala Ala Val Ser Val Ile Thr Pro Val
 210 215 220

Gly Met Asp His Val Asp Arg Leu Gly Asn Thr Ile Gly Glu Ile Ala
 225 230 235 240

Gly Glu Lys Ala Gly Ile Ile Lys Ala Arg Pro Ala Ser Glu Asp Gly
 245 250 255

Thr Glu Pro Glu Gly Asn Val Val Ile Val Gly Lys Gln Glu Pro Glu
 260 265 270

Ala Met Asn Val Ile Leu Gln Gln Ala Val Asp Val Asp Ala Ala Val
 275 280 285

Ala Arg Leu Asn Met Glu Phe Gly Val Val Glu Ser Ala Ile Ala Val

```
<210> 699
<211> 600
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(577)  
<223> RXA01517
```

```

<400> 699
tccataagcc caaagcaccg atcccacgta cttttgctga cgtcgcgggtg gttgcccgcac 60

gttccaggaa atccatggct gctggaagga gcaacgccta atg cat gca gtt ttg 115
                               Met His Ala Val Leu
                               1           5

tcc atc ggt tcc aac atg gat gat cgc tac gcg ctg ctc aac aca gtg 163
Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala Leu Leu Asn Thr Val

```

	10	15	20	
atc gag gaa ttc aaa gat gag atc gtg gcg cag tct gcg atc tac tca				211
Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser				
	25	30	35	
acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg				259
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val				
	40	45	50	
ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc				307
Leu Val Val Glu Val Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly				
	55	60	65	
caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg				355
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly				
	70	75	80	85
cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa				403
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu				
	90	95	100	
gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct				451
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala				
	105	110	115	
tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat				499
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp				
	120	125	130	
gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat				547
Ala Val Leu His Gly Thr Thr Ile Ala Glu His Val Asp Asn Leu Asp				
	135	140	145	
ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggttttcat				597
Pro Thr Asp Ile Glu Gly Val Thr Lys Ile				
	150	155		
gca				600

<210> 700

<211> 159

<212> PRT

<213> Corynebacterium glutamicum

<400> 700

Met	His	Ala	Val	Leu	Ser	Ile	Gly	Ser	Asn	Met	Asp	Asp	Arg	Tyr	Ala
1				5				10						15	

Leu	Leu	Asn	Thr	Val	Ile	Glu	Glu	Phe	Lys	Asp	Glu	Ile	Val	Ala	Gln
		20						25					30		

Ser	Ala	Ile	Tyr	Ser	Thr	Pro	Pro	Trp	Gly	Ile	Glu	Asp	Gln	Asp	Glu
		35					40					45			

Phe	Leu	Asn	Ala	Val	Leu	Val	Val	Glu	Val	Glu	Glu	Thr	Pro	Ile	Glu
	50					55					60				

Leu	Leu	Arg	Arg	Gly	Gln	Lys	Leu	Glu	Glu	Ala	Ala	Glu	Arg	Val	Arg
65					70					75					80

Val Arg Lys Trp Gly Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile
85 90 95

Ile Lys Asp Gly Glu Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu
100 105 110

Pro His Pro Trp Ala Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu
115 120 125

Glu Ala Glu Pro Asp Ala Val Leu His Gly Thr Thr Ile Ala Glu His
130 135 140

Val Asp Asn Leu Asp Pro Thr Asp Ile Glu Gly Val Thr Lys Ile
145 150 155

<210> 701

<211> 1983

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1960)

<223> RXA00579

<400> 701

tcgtctaagt ttttctttga gttttcatat gtagaaggca tcgtcggctt cggcctggcg 60

gtgcttttct cgttgttttg tggttttgtc agaggatgtc atg cgc gtt tta att 115
Met Arg Val Leu Ile
1 5

att gat aat tat gat tct ttc acg ttt aat ctc gcc acc tat gtg gaa 163
Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu
10 15 20

gag gtt acg ggt cag gca cct gtg gtg gtg cct aat gat caa gaa ata 211
Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile
25 30 35

gat gag atg ctt ttc gac gcc gtc atc ctc tca cct ggc ccg ggc cac 259
Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His
40 45 50

gcc ggc gtt gcg gct gat ttt ggt atc tgt gca ggc gtc att gag cgt 307
Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg
55 60 65

gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg 355
Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala
70 75 80 85

ttg gcc tat ggc ggt gat gtt gat ttg gcg ccc agg ccg gtc cac ggt 403
Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly
90 95 100

gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc 451
Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile
105 110 115

cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc 499
Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg
120 125 130

ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc 547
Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile
135 140 145

atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat 595
Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His
150 155 160 165

ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc 643
Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe
170 175 180

ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att 691
Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile
185 190 195

ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat 739
Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His
200 205 210

tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt 787
Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu
215 220 225

ggt gat gcc agc ggt cct ctc gca gcg aca aaa acc cat aat gtc ggc 835
Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly
230 235 240 245

gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca 883
Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser
250 255 260

gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt 931
Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly
265 270 275

tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt 979
Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser
280 285 290

ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa
1027
Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu
295 300 305

tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt
1075
Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe
310 315 320 325

gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct
1123
Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro
330 335 340

gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat
 1171
 Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr
 345 350 355

ctc gac aaa att cgc aga gcc cag gag ctg att act cgc ggc gaa tcg
 1219
 Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser
 360 365 370

tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc
 1267
 Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala
 375 380 385

cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat
 1315
 Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr
 390 395 400 405

ggt gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg
 1363
 Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro
 410 415 420

gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc
 1411
 Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro
 425 430 435

att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa
 1459
 Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu
 440 445 450

atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg
 1507
 Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu
 455 460 465

atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc
 1555
 Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro
 470 475 480 485

acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca
 1603
 Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr
 490 495 500

gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt
 1651
 Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser
 505 510 515

ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt
 1699
 Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly
 520 525 530

gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct
1747

Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala
535 540 545

cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc
1795

Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly
550 555 560 565

gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat
1843

Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn
570 575 580

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn
600 605 610

ttg ttt ggg gtt gaa ttc cca tgacgtacct cgtgtgggac ggt
1983

Leu Phe Gly Val Glu Phe Pro
615 620

<210> 702

<211> 620

<212> PRT

<213> Corynebacterium glutamicum

<400> 702

Met Arg Val Leu Ile Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu
1 5 10 15

Ala Thr Tyr Val Glu Glu Val Thr Gly Gln Ala Pro Val Val Val Pro
20 25 30

Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser
130 135 140

Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp
145 150 155 160

Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln
165 170 175

Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu
180 185 190

Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu
195 200 205

Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln
210 215 220

Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys
225 230 235 240

Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp
245 250 255

Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp
260 265 270

Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala
275 280 285

Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg
290 295 300

Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu
305 310 315 320

Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val
325 330 335

Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp
340 345 350

Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile
355 360 365

Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly
370 375 380

Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala
385 390 395 400

Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile
405 410 415

Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr
420 425 430

Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala
435 440 445

Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp

450	455	460
Arg Ala Glu Asn Leu Met	Ile Val Asp Leu Val	Arg Asn Asp Leu Ala
465	470	475 480
Arg Gly Ala Leu Pro Thr	Thr Val Lys Thr Ser Lys	Leu Phe Asp Val
485	490	495
Glu Thr Tyr Ala Thr Val	His Gln Leu Val Ser Thr	Val Ser Ala Glu
500	505	510
Leu Gly Pro Arg Ser Pro	Ile Glu Cys Val Arg Ala	Ala Phe Pro Gly
515	520	525
Gly Ser Met Thr Gly Ala	Pro Lys Leu Arg Thr Met	Glu Ile Ile Asp
530	535	540
Glu Leu Glu Ala Ala Pro	Arg Gly Ile Tyr Ser Gly	Gly Leu Gly Tyr
545	550	555 560
Phe Ser Leu Asp Gly Ala	Val Asp Leu Ser Met Val	Ile Arg Thr Leu
565	570	575
Val Ile Gln Asn Asn His	Val Glu Tyr Gly Val Gly	Gly Ala Leu Leu
580	585	590
Ala Leu Ser Asp Pro Glu	Ala Glu Trp Glu Glu Ile	Arg Val Lys Ser
595	600	605
Arg Pro Leu Leu Asn Leu	Phe Gly Val Glu Phe Pro	
610	615	620

<210> 703

<211> 747

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(724)

<223> RXA00958

<400> 703

attctaattcc tcaatctgaa gccgatgaga cggtgcacaa ggcgtatgcc gtgttgaatg 60

ccattgcgct	tgctgctggg	tccactttgg	aggatcatccg	atg	aca	cac	gtt	gtt	115
				Met	Thr	His	Val	Val	
				1				5	

ctc	att	gat	aat	cac	gat	tct	ttt	gtc	tac	aac	ctg	gtg	gat	gcg	ttc	163
Leu	Ile	Asp	Asn	His	Asp	Ser	Phe	Val	Tyr	Asn	Leu	Val	Asp	Ala	Phe	
			10					15					20			

gcc	gtg	gcc	ggg	tat	aag	tgc	acg	gtg	ttc	cgc	aat	acg	gtg	cca	gtg	211
Ala	Val	Ala	Gly	Tyr	Lys	Cys	Thr	Val	Phe	Arg	Asn	Thr	Val	Pro	Val	
			25					30					35			

gaa	acc	att	ttg	gca	gcc	aac	ccg	gac	ctg	atc	tgc	ctt	tca	cct	gga	259
Glu	Thr	Ile	Leu	Ala	Ala	Asn	Pro	Asp	Leu	Ile	Cys	Leu	Ser	Pro	Gly	
			40				45					50				

cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307
 Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg
 55 60 65

aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355
 Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala
 70 75 80 85

ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403
 Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His
 90 95 100

ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451
 Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro
 105 110 115

gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499
 Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile
 120 125 130

cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547
 Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val
 135 140 145

gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595
 Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile
 150 155 160 165

ggt gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643
 Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly
 170 175 180

ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691
 Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile
 185 190 195

ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744
 Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
 200 205

tca 747

<210> 704

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 704

Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn
1 5 10 15

Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg
20 25 30

Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile
35 40 45

Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met
50 55 60

Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys
65 70 75 80

Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro
85 90 95

Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala
100 105 110

Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro
115 120 125

Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His
130 135 140

Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr
145 150 155 160

Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp
165 170 175

Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro
180 185 190

Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
195 200 205

<210> 705
<211> 1266
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101) .. (1243)
<223> RXA02790

<400> 705

tggatgctcg cacccgagcc ctggaaccac aatccacaga caccgaagat ttcgacgaga 60

agggaattt cccaggatga accaaatccg aaaccgcccgg atg gag ccc gtc tac 115
Met Glu Pro Val Tyr
1 5

gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163
Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile
10 15 20

ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211
Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg
25 30 35

acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259
Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val
40 45 50

gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa	307
Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu	
55 60 65	
gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc	355
Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser	
70 75 80 85	
aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag	403
Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln	
90 95 100	
gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac	451
Glu Gln Met Asn Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp	
105 110 115	
aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac	499
Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp	
120 125 130	
gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc	547
Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile	
135 140 145	
gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag	595
Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu	
150 155 160 165	
gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc	643
Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val	
170 175 180	
cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag	691
Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys	
185 190 195	
cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc	739
Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser	
200 205 210	
aac gac gcc cag gga atc ctc acc gat ctg atc acg cga tca gca aac	787
Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn	
215 220 225	
cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt	835
His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu	
230 235 240 245	
act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca	883
Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu Ile Glu Arg Glu Ala	
250 255 260	
cca gca gga gat ttt gat aag gtc gcc cgc gtc atc ttg aac cgt ctc	931
Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu	
265 270 275	
gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg	979
Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu	
280 285 290	

tct gaa caa gaa gta gca acc acc gac gaa gac cgt cag acc gtc acc
1027

Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp Arg Gln Thr Val Thr
295 300 305

cca tgg aac act tac gcc atg gac ggc ctg cca caa acc ccc atc gcc
1075

Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro Gln Thr Pro Ile Ala
310 315 320 325

gca gta tcc acc gaa gca ctc caa gcc atg gaa aac cct gca gaa gga
1123

Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu Asn Pro Ala Glu Gly
330 335 340

aac tgg ctg tac ttt gtc acc atc gac acc gat gga acc acc gtg ttc
1171

Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp Gly Thr Thr Val Phe
345 350 355

aac gac acc ttc gaa gag cac gaa gcc gac att gag caa gct ttg aac
1219

Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile Glu Gln Ala Leu Asn
360 365 370

agt ggc gtt cta gac agc aac cga taaggatcag cgaataaaaat tgg
1266

Ser Gly Val Leu Asp Ser Asn Arg
375 380

<210> 706

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 706

Met Glu Pro Val Tyr Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr
1 5 10 15

Ile Ala Ser Leu Ile Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val
20 25 30

Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly
35 40 45

Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu
50 55 60

Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe
65 70 75 80

Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly
85 90 95

Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Val Ser Ala
100 105 110

Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly
115 120 125

Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly
 130 135 140

Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn
 145 150 155 160

Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro
 165 170 175

Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg
 180 185 190

Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr
 195 200 205

Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile
 210 215 220

Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala
 225 230 235 240

Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu
 245 250 255

Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val
 260 265 270

Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr
 275 280 285

Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp
 290 295 300

Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro
 305 310 315 320

Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu
 325 330 335

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp
 340 345 350

Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile
 355 360 365

Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg
 370 375 380

<210> 707

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00106

<400> 707

tggagctcaa caaggcagcg tacatgtttg agtacagctt cgatgacatc accgtgtccg 60

gctacgatcc acaccattg atccgcggca aggtcgccgt atg atc ggt gcg att 115
Met Ile Gly Ala Ile
1 5

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
10 15 20

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
25 30 35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
40 45 50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
55 60 65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355
Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
70 75 80 85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
90 95 100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
105 110 115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
120 125 130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
135 140 145

atc aag gtt taaggagcaa acaacatgag caa 579
Ile Lys Val
150

<210> 708

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 708

Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp
1 5 10 15Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
20 25 30Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
35 40 45

Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
50 55 60

Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
65 70 75 80

Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
85 90 95

Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
100 105 110

Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
115 120 125

Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
130 135 140

Lys Phe Gln Arg Tyr Ile Lys Val
145 150

<210> 709

<211> 2599

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2599)

<223> RXN02198

<400> 709

agactagtggt cgctttgcct gtgttgctta ggcggcggtg aaaatgaact acgaatgaaa 60

agttcgggaa ttgtctaatac cgtactaagc tgtctacaca atg tct act tca gtt 115
Met Ser Thr Ser Val
1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
25 30 35

caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259
Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
40 45 50

tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
55 60 65

cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act 355
His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
70 75 80 85

ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt 403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg

90										95										100									
tgc	cgt	gag	ctt	gcc	tac	aag	ggc	act	gca	gtg	gct	agg	gaa	gtg	gct					451									
Cys	Arg	Glu	Leu	Ala	Tyr	Lys	Gly	Thr	Ala	Val	Ala	Arg	Glu	Val	Ala														
			105					110					115																
gat	gag	atg	ggg	ccg	ggc	cga	aac	ggc	atg	cgg	cgt	ttc	gtg	gtt	ggt					499									
Asp	Glu	Met	Gly	Pro	Gly	Arg	Asn	Gly	Met	Arg	Arg	Phe	Val	Val	Gly														
		120					125					130																	
tcc	ctg	gga	ctt	gga	acg	aag	ctt	cca	tcg	ctg	ggc	cat	gca	ccg	tat					547									
Ser	Leu	Gly	Pro	Gly	Thr	Lys	Leu	Pro	Ser	Leu	Gly	His	Ala	Pro	Tyr														
		135				140					145																		
gca	gat	ttg	cgt	ggg	cac	tac	aag	gaa	gca	gcg	ctt	ggc	atc	atc	gac					595									
Ala	Asp	Leu	Arg	Gly	His	Tyr	Lys	Glu	Ala	Ala	Leu	Gly	Ile	Ile	Asp														
150					155				160						165														
ggt	ggt	ggc	gat	gcc	ttt	ttg	att	gag	act	gct	cag	gac	ttg	ctt	cag					643									
Gly	Gly	Gly	Asp	Ala	Phe	Leu	Ile	Glu	Thr	Ala	Gln	Asp	Leu	Leu	Gln														
				170					175					180															
gtc	aag	gct	gcg	gtt	cac	ggc	gtt	caa	gat	gcc	atg	gct	gaa	ctt	gat					691									
Val	Lys	Ala	Ala	Val	His	Gly	Val	Gln	Asp	Ala	Met	Ala	Glu	Leu	Asp														
			185					190					195																
aca	ttc	ttg	ccc	att	att	tgc	cac	gtc	acc	gta	gag	acc	acc	ggc	acc					739									
Thr	Phe	Leu	Pro	Ile	Ile	Cys	His	Val	Thr	Val	Glu	Thr	Thr	Gly	Thr														
		200				205						210																	
atg	ctc	atg	ggt	tct	gag	atc	ggt	gcc	gcg	ttg	aca	gcg	ctg	cag	cca					787									
Met	Leu	Met	Gly	Ser	Glu	Ile	Gly	Ala	Ala	Leu	Thr	Ala	Leu	Gln	Pro														
		215				220					225																		
ctg	ggt	atc	gac	atg	att	ggt	ctg	aac	tgc	gcc	acc	ggc	cca	gat	gag					835									
Leu	Gly	Ile	Asp	Met	Ile	Gly	Leu	Asn	Cys	Ala	Thr	Gly	Pro	Asp	Glu														
230					235				240					245															
atg	agc	gag	cac	ctg	cgt	tac	ctg	tcc	aag	cac	gcc	gat	att	cct	gtg					883									
Met	Ser	Glu	His	Leu	Arg	Tyr	Leu	Ser	Lys	His	Ala	Asp	Ile	Pro	Val														
			250						255				260																
tgc	gtg	atg	ctt	ggc	tac	aag	ggc	act	gca	gtg	gct	agg	gaa	gtg	gct					931									
Ser	Val	Met	Pro	Asn	Ala	Gly	Leu	Pro	Val	Leu	Gly	Lys	Asn	Gly	Ala														
		265						270					275																
gaa	tac	cca	ctt	gag	gct	gag	gat	ttg	gcg	cag	gcg	ctg	gct	gga	ttc					979									
Glu	Tyr	Pro	Leu	Glu	Ala	Glu	Asp	Leu	Ala	Gln	Ala	Leu	Ala	Gly	Phe														
		280					285					290																	
gtc	tcc	gaa	tat	ggc	ctg	tcc	atg	gtg	ggt	ggt	tgt	tgt	ggc	acc	aca														
1027																													
Val	Ser	Glu	Tyr	Gly	Leu	Ser	Met	Val	Gly	Gly	Cys	Cys	Gly	Thr	Thr														
		295				300					305																		
cct	gag	cac	atc	cgt	gcg	gtc	cgc	gat	gcg	gtg	gtt	ggt	gtt	cca	gag														
1075																													
Pro	Glu	His	Ile	Arg	Ala	Val	Arg	Asp	Ala	Val	Val	Gly	Val	Pro	Glu														
310					315					320																			

cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag
1123

Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln
330 335 340

gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc
1171

Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr
345 350 355

tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc
1219

Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg
360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc
1267

Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly
375 380 385

gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt
1315

Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly
390 395 400 405

gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc
1363

Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr
410 415 420

gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg
1411

Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu
425 430 435

cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt
1459

Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu
440 445 450

gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac
1507

Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp
455 460 465

ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag
1555

Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys
470 475 480 485

cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag
1603

Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln
490 495 500

gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac
1651

Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp
505 510 515

gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac
1699

Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp
520 525 530

tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat
1747

Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp
535 540 545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca
1795

Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro
550 555 560 565

gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac
1843

Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn
570 575 580

cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att
1891

Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile
585 590 595

gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg
1939

Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro
600 605 610

atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc
1987

Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val
615 620 625

tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag
2035

Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln
630 635 640 645

ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa
2083

~~Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu~~
650 655 660

cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc
2131

Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile
665 670 675

gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag
2179

Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys
680 685 690

gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg
2227

Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met
695 700 705

aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc
2275

Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe
710 715 720 725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa
2323

Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu
730 735 740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag
2371

Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu
745 750 755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat
2419

Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp
760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac
2467

Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
775 780 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca
2515

Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala
790 795 800 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg
2563

Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val
810 815 820

aag tcc acc gtg gtg atg aag caa acc atc agc gac
2599

Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser Asp
825 830

<210> 710

<211> 833

<212> PRT

<213> Corynebacterium glutamicum

<400> 710

Met Ser Thr Ser Val Thr Ser Pro Ala His Asn Asn Ala His Ser Ser
1 5 10 15

Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala
20 25 30

Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe
35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
65 70 75 80

Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
 85 90 95
 Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
 100 105 110
 Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
 115 120 125
 Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
 130 135 140
 Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
 145 150 155 160
 Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
 165 170 175
 Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
 180 185 190
 Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
 195 200 205
 Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu
 210 215 220
 Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala
 225 230 235 240
 Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His
 245 250 255
 Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu
 260 265 270
 Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln
 275 280 285
 Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly
 290 295 300
 Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val
 305 310 315 320
 Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala
 325 330 335
 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val
 340 345 350
 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser
 355 360 365
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu
 370 375 380
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln
 385 390 395 400

Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
 405 410 415
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
 420 425 430
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
 435 440 445
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
 450 455 460
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
 500 505 510
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
 515 520 525
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu
 530 535 540
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
 545 550 555 560
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
 565 570 575
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
 580 585 590
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
 595 600 605
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
 610 615 620
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
 625 630 635 640
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys
 645 650 655
 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
 660 665 670
 Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
 675 680 685
 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
 690 695 700
 Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
 705 710 715 720
 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala

	725		730		735
Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly					
	740		745		750
Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys					
	755		760		765
Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser					
	770		775		780
Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser					
	785		790		800
Ala Met Leu Glu Ala Ala Glu Glu His Lys Ala Asp Val Ile Gly Met					
	805		810		815
Ser Gly Leu Leu Val Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser					
	820		825		830

Asp

<210> 711
 <211> 2578
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2578)
 <223> FRXA02198

<400> 711
 agactagtggtg cgctttgcct gtgttgctta ggcggcggttg aaaatgaact acgaatgaaa 60
 agttcggggaa ttgtctaatac cgtactaagc tgtctacaca atg tct act tca gtt 115
 Met Ser Thr Ser Val
 1 5
 act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
 25 30 35

caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259
 Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
 40 45 50

tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307
 Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
 55 60 65

cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act 355
 His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
 70 75 80 85

ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt 403
 Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg
 90 95 100

tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct 451
 Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala
 105 110 115

gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt 499
 Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly
 120 125 130

tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat 547
 Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr
 135 140 145

gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac 595
 Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp
 150 155 160 165

ggt ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag 643
 Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln
 170 175 180

gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat 691
 Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp
 185 190 195

aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc 739
 Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr
 200 205 210

atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca 787
 Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro
 215 220 225

ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag 835
 Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu
 230 235 240 245

atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg 883
 Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val
 250 255 260

tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca 931
 Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala
 265 270 275

gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc 979
 Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe
 280 285 290

gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca
 1027
 Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr
 295 300 305

cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag
 1075
 Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu
 310 315 320 325

cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag
1123

Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln
330 335 340

gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc
1171

Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr
345 350 355

tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc
1219

Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg
360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc
1267

Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly
375 380 385

gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt
1315

Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly
390 395 400 405

gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc
1363

Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr
410 415 420

gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg
1411

Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu
425 430 435

cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt
1459

Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu
440 445 450

gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac
1507

Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp
455 460 465

ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag
1555

Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys
470 475 480 485

cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag
1603

Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln
490 495 500

gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac
1651

Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp
505 510 515

gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac
1699

Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp
520 525 530

tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat
1747

Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp
535 540 545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca
1795

Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro
550 555 560 565

gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac
1843

Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn
570 575 580

cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att
1891

Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile
585 590 595

gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg
1939

Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro
600 605 610

atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc
1987

Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val
615 620 625

tat gat cgc cgc acc gag gat tac gat ccg ctc cag gaa ttc atg cag
2035

Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln
630 635 640 645

ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa
2083

Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu
650 655 660

cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc
2131

Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile
665 670 675

gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag
2179

Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys
680 685 690

gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg
2227

Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met
695 700 705

aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc
2275

Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe
710 715 720 725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa
2323

Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu
730 735 740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag
2371

Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu
745 750 755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat
2419

Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp
760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac
2467

Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
775 780 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca
2515

Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala
790 795 800 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg
2563

Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val
810 815 820

aag tcc acc gtg gtg
2578

Lys Ser Thr Val Val
825

<210> 712

~~<211> 826~~

<212> PRT

<213> Corynebacterium glutamicum

<400> 712

Met Ser Thr Ser Val Thr Ser Pro Ala His Asn Asn Ala His Ser Ser
1 5 10 15

Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala
20 25 30

Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe
35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
65 70 75 80

999

Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
 405 410 415
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
 420 425 430
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
 435 440 445
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
 450 455 460
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
 500 505 510
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
 515 520 525
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu
 530 535 540
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
 545 550 555 560
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
 565 570 575
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
 580 585 590
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
 595 600 605
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
 610 615 620
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
 625 630 635 640
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys
 645 650 655
 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
 660 665 670
 Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
 675 680 685
 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
 690 695 700
 Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
 705 710 715 720
 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala

725	730	735
Val Ala Tyr Leu Glu Pro Phe Met	Glu Glu Glu Ala Glu Ala Thr Gly	
740	745	750
Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys		
755	760	765
Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser		
770	775	780
Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser		
785	790	800
Ala Met Leu Glu Ala Ala Glu Glu His Lys Ala Asp Val Ile Gly Met		
805	810	815
Ser Gly Leu Leu Val Lys Ser Thr Val Val		
820	825	
 <210> 713		
<211> 2358		
<212> DNA		
<213> Corynebacterium glutamicum		
 <220>		
<221> CDS		
<222> (101)..(2335)		
<223> RXN02085		
 <400> 713		
caccgcggtga ttctgcgaac cttgaaacat cgtcagaaga ttgccgtgcg tcctagccgg 60		
gatccgcacg ttcgggtcaa gcagaaagtc tttaactcac atg act tcc aac ttt		115
	Met Thr Ser Asn Phe	
	1	5
tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg		163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu		
10	15	20
aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa		211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu		
25	30	35
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg		259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu		
40	45	50
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca		307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala		
55	60	65
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat		355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp		
70	75	80
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc		403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg		
90	95	100

tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg	451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
105 110 115	
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct	499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
120 125 130	
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc	547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
135 140 145	
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt	595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
150 155 160 165	
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct	643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	
170 175 180	
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc	739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc	835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc	883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
250 255 260	
gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt	931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
280 285 290	
acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc	
1027	
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
295 300 305	
ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac	
1075	
Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
310 315 320 325	
acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc	
1123	

Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala
 330 335 340
 ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta
 1171
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
 345 350 355
 gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att
 1219
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
 360 365 370
 gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc
 1267
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
 375 380 385
 cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag
 1315
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
 390 395 400 405
 aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc
 1363
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
 410 415 420
 cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa
 1411
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
 425 430 435
 tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat
 1459
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
 440 445 450
 ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac
 1507
 Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
 455 460 465
 ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc
 1555
 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
 470 475 480 485
 gac ggt ttc ctc tca acc gcc aac gcc tgg gtc caa agc tac gcc tcc
 1603
 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
 490 495 500
 cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg
 1651
 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
 505 510 515
 cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag
 1699
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys

520	525	530
cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc 1747		
His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser 535 540 545		
ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca 1795		
Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala 550 555 560 565		
ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag 1843		
Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys 570 575 580		
atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccg cta cga 1891		
Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg 585 590 595		
gac gtc gat aag cct gcc tac ctg cag tgg tcc gtg gac tcc ttc cgc 1939		
Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg 600 605 610		
ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg 1987		
Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met 615 620 625		
tgc tac tcc gag ttc aac gaa gtg atc tcc tcg gtc atc gcg ttg gat 2035		
Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp 630 635 640 645		
gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc 2083		
Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu 650 655 660		
gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gta 2131		
Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val 665 670 675		
tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt 2179		
Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly 680 685 690		
ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc 2227		
Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val 695 700 705		
aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct 2275		
Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala 710 715 720 725		

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc
2323

Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile
730 735 740

gga gca act atc taaattgggt taccgctagg aac
2358

Gly Ala Thr Ile
745

<210> 714

<211> 745

<212> PRT

<213> Corynebacterium glutamicum

<400> 714

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
180 185 190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
195 200 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
210 215 220

Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr

225		230		235		240
Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly	245		250		255	
Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu	260		265		270	
Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly	275		280		285	
Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys	290		295		300	
Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu	305		310		315	320
Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val	325		330		335	
Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu	340		345		350	
Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala	355		360		365	
Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro	370		375		380	
Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg	385		390		395	400
Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr	405		410		415	
Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala	420		425		430	
Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met	435		440		445	
Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu	450		455		460	
Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr	465		470		475	480
Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val	485		490		495	
Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn	500		505		510	
Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln	515		520		525	
Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr	530		535		540	
Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr	545		550		555	560

Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
 565 570 575

Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
 580 585 590

Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser
 595 600 605

Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
 610 615 620

Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser
 625 630 635 640

Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
 645 650 655

Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
 660 665 670

Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala
 675 680 685

Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro
 690 695 700

Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp
 705 710 715 720

Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln
 725 730 735

Ala Arg Glu Lys Ile Gly Ala Thr Ile
 740 745

<210> 715

<211> 1923

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1900)

<223> FRXA02085

<400> 715

caccgcgtga ttctgcgaac cttgaaacat cgtcagaaga ttgccgtgcg tcctagccgg 60

gatccgcacg ttccggtcaa gcagaaagtc tttaactcac atg act tcc aac ttt 115
 Met Thr Ser Asn Phe
 1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163
 Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
 10 15 20

aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa 211
 Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu

25	30	35	
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tgc gat tct ttg Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu 40 45 50			259
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala 55 60 65			307
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp 70 75 80 85			355
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg 90 95 100			403
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met 105 110 115			451
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser 120 125 130			499
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu 135 140 145			547
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly 150 155 160 165			595
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro 170 175 180			643
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys 185 190 195			691
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr 200 205 210			739
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr 215 220 225			787
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly 230 235 240 245			835
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly 250 255 260			883
gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly 265 270 275			931

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc
 1027
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac
 1075
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc
 1123
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta
 1171
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att
 1219
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc
 1267
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag
 1315
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
 390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc
 1363
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
 410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa
 1411
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat
 1459
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
 440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac
 1507
 Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
 455 460 465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc
1555

Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
470 475 480 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc
1603

Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg
1651

Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag
1699

Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc
1747

His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca
1795

Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
550 555 560 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag
1843

Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
570 575 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg
1891

Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr
585 590 595

aga cgt cga taagcctgcc tacctgcagt ggt
1923

Arg Arg Arg
600

<210> 716

<211> 600

<212> PRT

<213> Corynebacterium glutamicum

<400> 716

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
 50 55 60
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
 65 70 75 80
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
 100 105 110
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
 115 120 125
 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
 145 150 155 160
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
 355 360 365
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro

```

370          375          380
Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
385          390          395          400
Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
          405          410          415
Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
          420          425          430
Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
          435          440          445
Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
          450          455          460
Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
465          470          475          480
Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
          485          490          495
Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
          500          505          510
Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
          515          520          525
Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
          530          535          540
Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
545          550          555          560
Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
          565          570          575
Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
          580          585          590
Leu Leu Pro Ala Thr Arg Arg Arg
          595          600

```

<210> 717
 <211> 603
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(580)
 <223> FRXA02086

<400> 717
 gatgatcagc cgctggctac cactgctgac caggttgac tggcactgcg cgatgaaatt 60

aacgatctca tcgaggctgg cgcaagatc atccaggtgg atg agc ctg cga ttc 115
 Met Ser Leu Arg Phe
 1 5

gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag 163
Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
10 15 20

tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac 211
Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
25 30 35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa gtg atc 259
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
40 45 50

tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
55 60 65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
70 75 80 85

ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403
Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
90 95 100

tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg 451
Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
105 110 115

gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
120 125 130

gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547
Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
135 140 145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600
Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
150 155 160

aac 603

<210> 718

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 718

Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
1 5 10 15

Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
20 25 30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
35 40 45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
50 55 60

Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
 65 70 75 80
 Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
 85 90 95
 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
 100 105 110
 Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
 115 120 125
 Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
 130 135 140
 Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
 145 150 155 160

<210> 719
 <211> 1326
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1303)
 <223> RXN02648

<400> 719
 atgaataaaa ttccgggtgc agtgaccgta ggtgaggttaa acgcggttag agtcgaatga 60
 gagtttgata cttttctttcg acttttagat tggattttca atg agc cag aac cgc 115
 Met Ser Gln Asn Arg
 1 5
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
 10 15 20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403

Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
 90 95 100

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
 105 110 115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 150 155 160 165

ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
 185 190 195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca ccg 787
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro
 215 220 225

gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag 835
 Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys
 230 235 240 245

gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca 883
 Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala
 250 255 260

gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc 931
 Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly
 265 270 275

tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att 979
 Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile
 280 285 290

ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca
 1027
 Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala
 295 300 305

tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt
 1075
 Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu
 310 315 320 325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac
1123

Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn
330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc
1171

Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg
1219

Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta
1267

Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac
1313

Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
390 395 400

aacgagggtt gct
1326

<210> 720

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 720

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg
 340 345 350
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
 370 375 380
 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
 385 390 395 400

Phe

<210> 721
 <211> 548
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(525)

<223> FRXA02648

<400> 721

```

gac gca ccg gac ttg gca gaa gca tgg gat cag atc aac cca gag cca 48
Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1             5             10             15

agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
             20             25             30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
             35             40             45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
             50             55             60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
             65             70             75             80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
             85             90             95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
             100             105             110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
             115             120             125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
             130             135             140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
             145             150             155             160

```

```

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
             165             170             175

```

```

taagctagac aacgagggtt gct 548

```

<210> 722

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 722

```

Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1             5             10             15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
             20             25             30

```

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
165 170 175

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
55 60 65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
 90 95 100
 gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
 105 110 115
 cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130
 ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145
 cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 150 155 160 165
 ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180
 gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
 185 190 195
 act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210
 tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
 215 220 225

<210> 724

<211> 228

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 724

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
 1 5 10 15
 Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30
 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn

```
<210> 725
<211> 551
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (1) .. (528)
<223> RXS02197
```

<400> 725																
gcc	gaa	cgc	atg	cgc	ttt	agc	ttc	cca	cgc	cag	cag	cgc	ggc	agg	ttc	48
Ala	Glu	Arg	Met	Arg	Phe	Ser	Phe	Pro	Arg	Gln	Gln	Arg	Gly	Arg	Phe	
1				5					10					15		
ttg	tgc	atc	gcg	gat	ttc	att	cgc	cca	cgc	gag	caa	gct	gtc	aag	gac	96
Leu	Cys	Ile	Ala	Asp	Phe	Ile	Arg	Pro	Arg	Glu	Gln	Ala	Val	Lys	Asp	
			20					25					30			
ggc	caa	gtg	gac	gtc	atg	cca	ttc	cag	ctg	gtc	acc	atg	ggg	aat	cct	144
Gly	Gln	Val	Asp	Val	Met	Pro	Phe	Gln	Leu	Val	Thr	Met	Gly	Asn	Pro	
		35					40					45				
att	gct	gat	ttc	gcc	aac	gag	ttg	ttc	gca	gcc	aat	gaa	tac	cgc	gag	192
Ile	Ala	Asp	Phe	Ala	Asn	Glu	Leu	Phe	Ala	Ala	Asn	Glu	Tyr	Arg	Glu	
	50					55					60					
tac	ttg	gaa	gtt	cac	ggc	atc	ggc	gtg	cag	ctc	acc	gaa	gca	ttg	gcc	240

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80
 gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt 288
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95
 gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110
 ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct 384
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125
 gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt 432
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
 130 135 140
 atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc 480
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
 145 150 155 160
 aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc 528
 Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
 165 170 175
 taacaccttt gagagggaact act 551

<210> 726

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 726

Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
 1 5 10 15
 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
 20 25 30
 Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
 35 40 45
 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
 50 55 60
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg

ggg ctg ctt acc acg cag cac agc taagctttaa ggccctccgg ggc 546
 Gly Leu Leu Thr Thr Gln His Ser
 135 140

<210> 728

<211> 141

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 728

Met Ser Lys Arg Glu Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly
 1 5 10 15

His Asp Pro Leu Lys Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala
 20 25 30

Gly Thr Leu Val Met Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val
 35 40 45

Ile Leu Arg Val Asp Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val
 50 55 60

Tyr Val Ser Ala Val Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln
 65 70 75 80

Arg Phe Ser Trp Ser Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala
 85 90 95

Leu Ala Gly Phe Phe Val His Pro Ala Met Gly Phe Ala Ala Ile Ile
 100 105 110

Phe Ile Ile Ala Trp Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile
 115 120 125

Asp Arg Met Lys Arg Gly Leu Leu Thr Thr Gln His Ser
 130 135 140

<210> 729

<211> 597

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(574)

<223> RXC01518

<400> 729

agcagaacct gatgccgtcc tgcacggcac gaccattgca gaacatgtgg ataattctga 60

tcccacagac attgaagggtg tcaccaagat ttaaggagtc gtg gct ttc atg cag 115
 Val Ala Phe Met Gln
 1 5

aaa acg tca gcg ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163
 Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala
 10 15 20

gtg tcc gcc att ttg acg tgg cgt ttt tat gga tcc atg acc tct att 211

Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile
 25 30 35

 tcc atc acg gta tcc atc act ttt tgg ttg ttg gcc gtg gtg tgt ggt 259
 Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly
 40 45 50

 ttc gca ggt gtg aag gtc caa ggt cgc ctc gat gag ggg ctg atc ggc 307
 Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Glu Gly Leu Ile Gly
 55 60 65

 cag gac aaa tcc caa atg aac ccc gtg acc att gcc tat ctg gcc atg 355
 Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met
 70 75 80 85

 ctg ggt cga gcg tgt gcg tgg ggt ggc gca att ttc ggc ggc gtt tat 403
 Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile Phe Gly Gly Val Tyr
 90 95 100

 gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag ttg tcc gca 451
 Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Glu Leu Ser Ala
 105 110 115

 gca tcg aat gat ctt ccg gga gtt att gcc tgt gcg ctg ggc gga atc 499
 Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile
 120 125 130

 gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg 547
 Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg Ser Cys Glu Ala Pro
 135 140 145

 cct ccc caa tct ggc gaa gcg atc agc tagattggaa ttcattgaatc 594
 Pro Pro Gln Ser Gly Glu Ala Ile Ser
 150 155

 aag 597

<210> 730

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 730

Val Ala Phe Met Gln Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly
 1 5 10 15

 Gly Phe Leu Ala Ala Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly
 20 25 30

 Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu
 35 40 45

 Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp
 50 55 60

 Glu Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile
 65 70 75 80

 Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile
 85 90 95

Phe Gly Gly Val Tyr Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala
100 105 110

Gly Glu Leu Ser Ala Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys
115 120 125

Ala Leu Gly Gly Ile Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg
130 135 140

Ser Cys Glu Ala Pro Pro Pro Gln Ser Gly Glu Ala Ile Ser
145 150 155

<210> 731

<211> 723

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(700)

<223> RXC01942

<400> 731

gccgcgaaaat tcggtgaaat tgaaggtatt cctgcagatc aggcaaattc ttccacgact 60

gtgatcaagg tcaacggcaa gaacgagtaa cctgggatcc atg ttg cgc att gga 115
Met Leu Arg Ile Gly
1 5

cta aca gga ggg atc ggc agc ggt aaa tct acc gtt gcc gat ctt ttg 163
Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr Val Ala Asp Leu Leu
10 15 20

tca tct gaa gga ttt ctc atc gtc gac gcg gac caa gtt gcc cgc gat 211
Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp Gln Val Ala Arg Asp
25 30 35

atc gtc gaa ccc gga caa ccg gca tta gca gag cta gct gaa gct ttt 259
Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu Leu Ala Glu Ala Phe
40 45 50

ggc caa gac atc tta aaa ccc gac ggc act cta gac cgc gcg gga tta 307
Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu Asp Arg Ala Gly Leu
55 60 65

gca gcc aaa gca ttt gtc agc gaa gaa caa aca gcg ctg ctc aat gcc 355
Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr Ala Leu Leu Asn Ala
70 75 80 85

att acc cac cct cgt atc gcc gaa gag tca gct cgt cga ttc aac gaa 403
Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala Arg Arg Phe Asn Glu
90 95 100

gcc gaa gat caa ggc gcc aaa gtt gcg gtt tat gac atg cct ttg ctt 451
Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr Asp Met Pro Leu Leu
105 110 115

gta gaa aaa ggc ctt gac cgc aag atg gac ctt gtc gtc gta gtt gat 499
Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu Val Val Val Val Asp

120	125	130	
gtt gac gta gag gaa cgc gtc cgc aga ctt gtg gaa aaa cgt ggc ctc			547
Val Asp Val Glu Glu Arg Val Arg Arg Leu Val Glu Lys Arg Gly Leu			
135	140	145	
aca gag gac gac gtg cgg cgt cga atc gct tct caa gtg ccc gac gac			595
Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser Gln Val Pro Asp Asp			
150	155	160	165
gtc aga ctt aaa gcc gct gac atc gtt gtg gac aat aac ggc acg cta			643
Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp Asn Asn Gly Thr Leu			
170	175	180	
gag gac ctt cat gct gaa gca agc aag ctg att gct gag att ctt agt			691
Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile Ala Glu Ile Leu Ser			
185	190	195	
cgc gtg aat tagcactaaa acatcgtcaa agt			723
Arg Val Asn			
200			

<210> 732

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 732

Met Leu Arg Ile Gly Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr			
1	5	10	15
Val Ala Asp Leu Leu Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp			
20	25	30	
Gln Val Ala Arg Asp Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu			
35	40	45	
Leu Ala Glu Ala Phe Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu			
50	55	60	
Asp Arg Ala Gly Leu Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr			
65	70	75	80
Ala Leu Leu Asn Ala Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala			
85	90	95	
Arg Arg Phe Asn Glu Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr			
100	105	110	
Asp Met Pro Leu Leu Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu			
115	120	125	
Val Val Val Val Asp Val Asp Val Glu Glu Arg Val Arg Arg Leu Val			
130	135	140	
Glu Lys Arg Gly Leu Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser			
145	150	155	160
Gln Val Pro Asp Asp Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp			
165	170	175	

Asn Asn Gly Thr Leu Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile
180 185 190

Ala Glu Ile Leu Ser Arg Val Asn
195 200

<210> 733

<211> 1194

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1171)

<223> RXN02802

<400> 733

ccttcgccgc ctgctccgac ctgcgccgacg ccgtcaaagc ccaggtcccg atctggaaag 60

agcaaacgcg cctcgacggc tccaccgatt gggtcggcct gtg aaa aac ctc gac 115
Val Lys Asn Leu Asp
1 5

atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa 163
Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly Glu Ile Gly Gln Gln
10 15 20

aaa caa caa tcg ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc 211
Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser Val Ile Gly Ala Gly
25 30 35

ggc ctc ggg tca ccc gcc ctg ctc tac ctt gct ggc gct ggc gtc ggc 259
Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala Gly Ala Gly Val Gly
40 45 50

cac atc cac atc att gac gat gac ctc gtc gac ctc tcc aac ctc cac 307
His Ile His Ile Ile Asp Asp Asp Leu Val Asp Leu Ser Asn Leu His
55 60 65

cgc cag gtc att cac acc acc gct ggc gtt gga aca ccc aag gcc gag 355
Arg Gln Val Ile His Thr Thr Ala Gly Val Gly Thr Pro Lys Ala Glu
70 75 80 85

tcc gcg cgc gaa gca atg ctg gca ctg aac cct tcc gtt aaa gtg acg 403
Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro Ser Val Lys Val Thr
90 95 100

gtt tct gtc agg cga ctg gac tgg tca aat gca ctt tct gag ctg gca 451
Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala Leu Ser Glu Leu Ala
105 110 115

gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac 499
Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His
120 125 130

ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc cac gtc tgg gca 547
Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile Pro His Val Trp Ala
135 140 145

tcc atc ctg ggt ttc gac gcc caa ctc tcc gtc ttc cac gcc ggc cac 595
 Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val Phe His Ala Gly His
 150 155 160 165

ggc ccc atc tac gaa gac ctc ttc ccc acc ccg cca cca ccc gga tcc 643
 Gly Pro Ile Tyr Glu Asp Leu Phe Pro Thr Pro Pro Pro Gly Ser
 170 175 180

gtc cca tca tgt tcc caa gca ggc gtt ttg ggt cca gtt gtc ggc gta 691
 Val Pro Ser Cys Ser Gln Ala Gly Val Leu Gly Pro Val Val Gly Val
 185 190 195

atg ggc tcc gcg atg gcc atg gaa gcc ctg aaa atc atc acc ggc gtg 739
 Met Gly Ser Ala Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val
 200 205 210

ggc aca ccc ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc 787
 Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly
 215 220 225

acc tgg gaa tac atc ccc gtc gtc ggt tgc ccg gag gtg ctg gaa ccg 835
 Thr Trp Glu Tyr Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg
 230 235 240 245

gtg ctt ggg tct gct ggt gtt tgc ggg att tct ggc ggt ttt ggt gag 883
 Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu
 250 255 260

gtg ctc gat gtt cct cga gtt tcc gcg ctg gtt gac ggc gtt tgc ctc 931
 Val Leu Asp Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu
 265 270 275

atc gac gtc cgc gaa ccc tcc gaa ttc tcc gcc tac tcc atc ccc ggc 979
 Ile Asp Val Arg Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly
 280 285 290

gcg cac aac acc cca ctg tcc gcc atc cgc gaa ggc gcc atc cca ccc
 1027
 Ala His Asn Thr Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro
 295 300 305

tcc gtt tcc gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc
 1075
 Ser Val Ser Ala Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val
 310 315 320 325

cgc tcc gca caa gcc atc gca att tta gaa tcc gca ggc tac acc gga
 1123
 Arg Ser Ala Gln Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly
 330 335 340

atg agc agc ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggc
 1171
 Met Ser Ser Leu Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly
 345 350 355

taaaaccaag gcgttggtgcc acc
 1194

<210> 734

<211> 357

<212> PRT

<213> Corynebacterium glutamicum

<400> 734

Val Lys Asn Leu Asp Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly
 1 5 10 15

Glu Ile Gly Gln Gln Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser
 20 25 30

Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala
 35 40 45

Gly Ala Gly Val Gly His Ile His Ile Ile Asp Asp Asp Leu Val Asp
 50 55 60

Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly
 65 70 75 80

Thr Pro Lys Ala Glu Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro
 85 90 95

Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala
 100 105 110

Leu Ser Glu Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn
 115 120 125

Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile
 130 135 140

Pro His Val Trp Ala Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val
 145 150 155 160

Phe His Ala Gly His Gly Pro Ile Tyr Glu Asp Leu Phe Pro Thr Pro
 165 170 175

Pro Pro Pro Gly Ser Val Pro Ser Cys Ser Gln Ala Gly Val Leu Gly
 180 185 190

Pro Val Val Gly Val Met Gly Ser Ala Met Ala Met Glu Ala Leu Lys
 195 200 205

Ile Ile Thr Gly Val Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr
 210 215 220

Ser Ser Leu Asp Gly Thr Trp Glu Tyr Ile Pro Val Val Gly Ser Pro
 225 230 235 240

Glu Val Leu Glu Arg Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser
 245 250 255

Gly Gly Phe Gly Glu Val Leu Asp Val Pro Arg Val Ser Ala Leu Val
 260 265 270

Asp Gly Val Ser Leu Ile Asp Val Arg Glu Pro Ser Glu Phe Ser Ala
 275 280 285

Tyr Ser Ile Pro Gly Ala His Asn Thr Pro Leu Ser Ala Ile Arg Glu
 290 295 300

Gly Ala Ile Pro Pro Ser Val Ser Ala Gly Lys Glu Val Ile Val Tyr
305 310 315 320

Cys Ala Ala Gly Val Arg Ser Ala Gln Ala Ile Ala Ile Leu Glu Ser
325 330 335

Ala Gly Tyr Thr Gly Met Ser Ser Leu Asp Gly Gly Ile Glu Gly Trp
340 345 350

Leu Asp Ser Leu Gly
355

<210> 735

<211> 497

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (7)..(474)

<223> FRXA02802

<400> 735

tccgcgatg gcc atg gaa gcc ctg aaa atc atc acc ggc gtg ggc aca ccc 51
Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val Gly Thr Pro
1 5 10 15

ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc acc tgg gaa 99
Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Glu
20 25 30

tac atc ccc gtc gtc ggt tgc ccg gag gtg ctg gaa cgg gtg ctt ggg 147
Tyr Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg Val Leu Gly
35 40 45

tct gct ggt gtt tgc ggc att tct ggc ggt ttt ggt gag gtg ctc gat 195
Ser Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu Val Leu Asp
50 55 60

gtt cct cga gtt tcc gcg ctg gtt gac ggc gtt tgc ctc atc gac gtc 243
Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val
65 70 75

cgc gaa ccc tcc gaa ttc tcc gcc tac tcc atc ccc ggc gcg cac aac 291
Arg Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly Ala His Asn
80 85 90 95

acc cca ctg tcc gcc atc cgc gaa ggc gcc atc cca ccc tcc gtt tcc 339
Thr Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro Ser Val Ser
100 105 110

gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc cgc tcc gca 387
Ala Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val Arg Ser Ala
115 120 125

caa gcc atc gca att tta gaa tcc gca ggc tac acc gga atg agc agc 435
Gln Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly Met Ser Ser
130 135 140

ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggg taaaaccaag 484
 Leu Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly
 145 150 155

gcgttggtgcc acc 497

<210> 736

<211> 156

<212> PRT

<213> Corynebacterium glutamicum

<400> 736

Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val Gly Thr Pro Leu
 1 5 10 15

Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Glu Tyr
 20 25 30

Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg Val Leu Gly Ser
 35 40 45

Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu Val Leu Asp Val
 50 55 60

Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val Arg
 65 70 75 80

Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly Ala His Asn Thr
 85 90 95

Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro Ser Val Ser Ala
 100 105 110

Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val Arg Ser Ala Gln
 115 120 125

Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly Met Ser Ser Leu
 130 135 140

Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly
 145 150 155

<210> 737

<211> 535

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA00438

<400> 737

ccttcgccgc ctgctccgac ctgcgccgac ccgtcaaagc ccagggtccc atctggaaag 60

agcaaacgcg cctcgacggc tccaccgatt gggtcggcct gtg aaa aac ctc gac 115
 Val Lys Asn Leu Asp
 1 5

atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa 163
 Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly Glu Ile Gly Gln Gln
 10 15 20

aaa caa caa tgc ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc 211
 Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser Val Ile Gly Ala Gly
 25 30 35

ggc ctc ggc tca ccc gcc ctg ctc tac ctt gct ggc gct ggc gtc ggc 259
 Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala Gly Ala Gly Val Gly
 40 45 50

cac atc cac atc att gac gat gac ctc gtc gac ctc tcc aac ctc cac 307
 His Ile His Ile Ile Asp Asp Asp Leu Val Asp Leu Ser Asn Leu His
 55 60 65

cgc cag gtc att cac acc acc gct ggc gtt gga aca ccc aag gcc gag 355
 Arg Gln Val Ile His Thr Thr Ala Gly Val Gly Thr Pro Lys Ala Glu
 70 75 80 85

tcc gcg cgc gaa gca atg ctg gca ctg aac cct tcc gtt aaa gtg acg 403
 Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro Ser Val Lys Val Thr
 90 95 100

gtt tct gtc agg cga ctg gac tgg tca aat gca ctt tct gag ctg gca 451
 Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala Leu Ser Glu Leu Ala
 105 110 115

gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac 499
 Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His
 120 125 130

ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc 535
 Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile Pro
 135 140 145

<210> 738

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 738

Val Lys Asn Leu Asp Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly
 1 5 10 15

Glu Ile Gly Gln Gln Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser
 20 25 30

Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala
 35 40 45

Gly Ala Gly Val Gly His Ile His Ile Ile Asp Asp Asp Leu Val Asp
 50 55 60

Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly
 65 70 75 80

Thr Pro Lys Ala Glu Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro
 85 90 95

Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala
 100 105 110
 Leu Ser Glu Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn
 115 120 125
 Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile
 130 135 140
 Pro
 145

<210> 739
 <211> 579
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(556)
 <223> RXN00437

<400> 739
 ttcatcatgg cgctgcccgg ctccacgggt gcggcgcgcg atgccaccgc tgtcctcgac 60
 ccactcattg atcacatcac tggaactctg caaggccacc atg aac act gac ccc 115
 Met Asn Thr Asp Pro
 1 5
 gct tac gtc gcc gaa caa acc ggc aaa ctc atc gac gct ttc ctc acc 163
 Ala Tyr Val Ala Glu Gln Thr Gly Lys Leu Ile Asp Ala Phe Leu Thr
 10 15 20
 acc gac ccc ctc gaa ccg ctg ctc gac gcc gcc aaa aac ggc gtc tgc 211
 Thr Asp Pro Leu Glu Pro Leu Leu Asp Ala Ala Lys Asn Gly Val Cys
 25 30 35
 aca gag gcg atg ggc gcg ctg gtc acc ttc gaa ggc atc gtc cgc gac 259
 Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu Gly Ile Val Arg Asp
 40 45 50
~~cac gac ggc gcc gcc cgc gtc acc tcc ctg acc tac acc gag cat ccc 307~~
 His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr Tyr Thr Ala His Pro
 55 60 65
 acc gcg ccg cag gtc ctt tct gct gtc gcg gac tcc atc gtt gaa aaa 355
 Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp Ser Ile Val Glu Lys
 70 75 80 85
 cac ccg cgc acc cgc ctc tgg acc gcg cac cgc acc ggc gcc ttg aaa 403
 His Pro Arg Thr Arg Leu Trp Thr Ala His Arg Thr Gly Ala Leu Lys
 90 95 100
 atc ggt gac gcc gcc ttc ctc gtc gtc gcc gcc tcc gcc cac cgc gcc 451
 Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala Ser Ala His Arg Ala
 105 110 115
 gac gcc ttc gcc gcc tgc tcc gac ctc gcc gac gcc gtc aaa gcc cag 499
 Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp Ala Val Lys Ala Gln
 120 125 130

gtc ccg atc tgg aaa gag caa acg cgc ctc gac ggc tcc acc gat tgg 547
 Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp Gly Ser Thr Asp Trp
 135 140 145

gtc ggc ctg tgaaaaacct cgacatcgcc cgc 579
 Val Gly Leu
 150

<210> 740

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 740

Met Asn Thr Asp Pro Ala Tyr Val Ala Glu Gln Thr Gly Lys Leu Ile
 1 5 10 15

Asp Ala Phe Leu Thr Thr Asp Pro Leu Glu Pro Leu Leu Asp Ala Ala
 20 25 30

Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
 35 40 45

Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
 50 55 60

Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
 65 70 75 80

Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
 85 90 95

Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
 100 105 110

Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
 115 120 125

Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
 130 135 140

Gly Ser Thr Asp Trp Val Gly Leu
 145 150

<210> 741

<211> 383

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(360)

<223> FRXA00437

<400> 741

aaa aac ggc gtc tgc aca gag gcg atg ggc gcg ctg gtc acc ttc gaa 48
 Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
 1 5 10 15

ggc atc gtc cgc gac cac gac ggc ggc gcc cgc gtg acc tcc ctg acc 96
 Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
 20 25 30

tac acc gcg cat ccc acc gcg ccg cag gtc ctt tct gct gtc gcg gac 144
 Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
 35 40 45

tcc atc gtt gaa aaa cac ccg cgc acc cgc ctc tgg acc gcg cac cgc 192
 Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
 50 55 60

acc ggc gcc ttg aaa atc ggt gac gcc gcc ttc ctc gtc gtc gcc gcc 240
 Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
 65 70 75 80

tcc gcc cac cgc gcc gac gcc ttc gcc gcc tgc tcc gac ctc gcc gac 288
 Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
 85 90 95

gcc gtc aaa gcc cag gtc ccg atc tgg aaa gag caa acg cgc ctc gac 336
 Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
 100 105 110

ggc tcc acc gat tgg gtc ggc ctg tgaaaaacct cgacatcgcc cgc 383
 Gly Ser Thr Asp Trp Val Gly Leu
 115 120

<210> 742

<211> 120

<212> PRT

<213> Corynebacterium glutamicum

<400> 742

Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
 1 5 10 15

Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
 20 25 30

Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
 35 40 45

Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
 50 55 60

Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
 65 70 75 80

Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
 85 90 95

Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
 100 105 110

Gly Ser Thr Asp Trp Val Gly Leu
 115 120

```
<210> 743
<211> 591
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(568)  
<223> RXN00439
```

<400> 743																		60
ctgccaccgc agactgtctg atcaggatcc cggcgcggac tacgggtggag gaaaacgaca																		
tcgttaagat ttacccattc aactaacagg agttaattta atg agc gag ctc acc																		115
Met Ser Glu Leu Thr																		5
1																		
cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa																		163
His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys																		20
10																		
15																		
20																		
aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg																		211
Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg																		35
25																		
30																		
35																		
ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggc gac																		259
Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp																		50
40																		
45																		
50																		
gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg																		307
Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr																		65
55																		
60																		
65																		
ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act																		355
Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr																		85
70																		
75																		
80																		
85																		
gtg gat ttt ttt gag ctt act gat ggt gtt ccg att gag gct tcg gtg																		403
Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg Ile Glu Ala Ser Val																		100
90																		
95																		
100																		
aaa acg cgt ggg gtt act ggt gtg gaa atg gag gcg ttg acg gcc gtg																		451
Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu Ala Leu Thr Ala Val																		115
105																		
110																		
115																		
agc act gcg gcg ctg acg gta tac gac atg atc aag gct gtg gat aag																		499
Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile Lys Ala Val Asp Lys																		130
120																		
125																		
130																		
atg gcc gtg att gat ggc att cgt gtg ctg tcg aaa act ggc ggt aaa																		547
Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser Lys Thr Gly Gly Lys																		145
135																		
140																		
145																		
tct ggg gat tgg tct gtt cag tgacagctct gggtatcggt gcg																		591
Ser Gly Asp Trp Ser Val Gln																		
150																		
155																		

<210>	744
<211>	156
<212>	PRT

<213> Corynebacterium glutamicum

<400> 744

```

Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val
  1              5              10              15

Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly
          20              25              30

Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly
          35              40              45

Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met
          50              55              60

Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro
          65              70              75              80

Leu Gly Lys Ile Thr Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg
          85              90              95

Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu
          100              105              110

Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile
          115              120              125

Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser
          130              135              140

Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val Gln
          145              150              155

```

<210> 745

<211> 218

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(195)

<223> FRXA00439

<400> 745

```

act gat ggt gtt cgg att gag gct tcg gtg aaa acg cgt ggg gtt act      48
Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr
  1              5              10              15

ggt gtg gaa atg gag gcg ttg acg gcc gtg agc act gcg gcg ctg acg      96
Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr
          20              25              30

gta tac gac atg atc aag gct gtg gat aag atg gcc gtg att gat ggc      144
Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly
          35              40              45

att cgt gtg ctg tcg aaa act ggc ggt aaa tct ggg gat tgg tct gtt      192
Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val
          50              55              60

```

cag tgacagctct gggtatcggt gcg
Gln
65

218

<210> 746
<211> 65
<212> PRT
<213> Corynebacterium glutamicum

<400> 746
Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr
1 5 10 15

Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr
20 25 30

Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly
35 40 45

Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val
50 55 60

Gln
65

<210> 747
<211> 358
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(358)
<223> FRXA00442

<400> 747
ctgccaccgc agactgtctg atcaggatcc cggcgcgagac tacggtggag gaaaacgaca 60

tcgttaagat ttaccattc aactaacagg agttaattta atg agc gag ctc acc 115
Met Ser Glu Leu Thr
1 5

cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa 163
His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys
10 15 20

aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg 211
Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg
25 30 35

ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggg gac 259
Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp
40 45 50

gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg 307
Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr
55 60 65

ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act 355

Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr
 70 75 80 85

gtg
 Val

358

<210> 748

<211> 86

<212> PRT

<213> Corynebacterium glutamicum

<400> 748

Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val
 1 5 10 15

Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly
 20 25 30

Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly
 35 40 45

Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met
 50 55 60

Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro
 65 70 75 80

Leu Gly Lys Ile Thr Val
 85

<210> 749

<211> 582

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(559)

<223> RXA00440

<400> 749

cggtatacga catgatcaag gctgtggata agatggccgt gattgatggc attcgtgtgc 60

tgtcgaaaac tggcggtaaa tctggggatt ggtctgttca gtg aca gct ctg gtt 115
 Val Thr Ala Leu Val
 1 5

atc gtt gcg tcc act cgc gcc gct gcc ggg gtg tat gag gat cgc tct 163
 Ile Val Ala Ser Thr Arg Ala Ala Gly Val Tyr Glu Asp Arg Ser
 10 15 20

ggc cca att ttg gtg tgg tgg ctg cgt gca aaa ggt ttt gac aca ccc 211
 Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys Gly Phe Asp Thr Pro
 25 30 35

gcc ccc gtg atc gtg gcg gac gcc aac ctg ccc gca ttc ctg gac gag 259
 Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro Ala Phe Leu Asp Glu
 40 45 50

ctg gaa ttt ccg cag gta gta ctt att tca ggc ggc acc gga ctc acg 307
 Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly Gly Thr Gly Leu Thr
 55 60 65
 cct gat gac atc acc gtg gac act tta atc ccg cgc ctc gac aaa gaa 355
 Pro Asp Asp Ile Thr Val Asp Thr Leu Ile Pro Arg Leu Asp Lys Glu
 70 75 80 85
 atc ccc ggc atc gcc cac gct ttt tgg aat tac agc atg gac gcc gtc 403
 Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr Ser Met Asp Ala Val
 90 95 100
 ccg acc gca gta ttg tcg cgc acc gtc gcg ggc acc atc ggc ggc agt 451
 Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly Thr Ile Gly Gly Ser
 105 110 115
 ttc atc atg gcg ctg ccc ggc tcc acg ggt gcg gcg cgc gat gcc acc 499
 Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala Ala Arg Asp Ala Thr
 120 125 130
 gct gtc ctc gac cca ctc att gat cac atc act gga act ctg caa ggc 547
 Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr Gly Thr Leu Gln Gly
 135 140 145
 cac cat gaa cac tgaccccgct tacgtcgccg aac 582
 His His Glu His
 150

<210> 750

<211> 153

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 750

Val Thr Ala Leu Val Ile Val Ala Ser Thr Arg Ala Ala Ala Gly Val
 1 5 10 15
 Tyr Glu Asp Arg Ser Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys
 20 25 30
 Gly Phe Asp Thr Pro Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro
 35 40 45
 Ala Phe Leu Asp Glu Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly
 50 55 60
 Gly Thr Gly Leu Thr Pro Asp Asp Ile Thr Val Asp Thr Leu Ile Pro
 65 70 75 80
 Arg Leu Asp Lys Glu Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr
 85 90 95
 Ser Met Asp Ala Val Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly
 100 105 110
 Thr Ile Gly Gly Ser Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala
 115 120 125
 Ala Arg Asp Ala Thr Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr

130 135 140

Gly Thr Leu Gln Gly His His Glu His
145 150

<210> 751
<211> 1287
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1264)
<223> RXN00441

<400> 751
agccttggga gcggtgatta tgcttttggc tgtctatgtc ctcattcattg gagccatcgg 60
agcgttacga ttgttttcca aggtgagaaa ggtttaattg atg tct cgt tcg ccg 115
Met Ser Arg Ser Pro
1 5
gag caa cat ttg gca gaa att tca gcg ctg ctt ccc cca caa aag tcc 163
Glu Gln His Leu Ala Glu Ile Ser Ala Leu Leu Pro Pro Gln Lys Ser
10 15 20
acg ttc gtg aat ctg cgc gaa gcg ttg gga cgc cgc acg ttt tca gcg 211
Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg Arg Thr Phe Ser Ala
25 30 35
gtc act gcg cag tgg gat tcg cca cgt ttt gat aat tcc caa atg gat 259
Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp Asn Ser Gln Met Asp
40 45 50
ggc ttc gcg ctt ggc ccc tca cat ctt aac ggt ggc acc ttc gca gtc 307
Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly Gly Thr Phe Ala Val
55 60 65
ggg cca acc att ccc gct ggt cat gat cct gat cag tgg tac cca cga 355
Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp Gln Trp Tyr Pro Arg
70 75 80 85

ggc atc gaa aaa gac atc gcg ccg att atg acg ggt gcg cgc ctt cct 403
Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr Gly Ala Arg Leu Pro
90 95 100
aaa aac acc gcc gcg atc att cct gtg gag aaa acc aca ccg gga aat 451
Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys Thr Thr Pro Gly Asn
105 110 115
ttc gac gcc cca cag gta gaa atc ccc gcc acc ccg caa ggt cag ttc 499
Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr Pro Gln Gly Gln Phe
120 125 130
ata cgg ttg cag ggt tcg gat att act gcc ggc gac gag atc att cca 547
Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly Asp Glu Ile Ile Pro
135 140 145
gca ggt acg gag ctt aac tcg gtg cac atc ggg gtg ttg gct agt cag 595
Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly Val Leu Ala Ser Gln

150	155	160	165	
tcg atc aag agc att gaa gtc gca gca aag cca cgt gtc ctc atc atc				643
Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro Arg Val Leu Ile Ile				
	170	175	180	
acc ggc ggg tct gaa att tca gaa cag cac gga ccc gcc acg atc cct				691
Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly Pro Ala Thr Ile Pro				
	185	190	195	
gat gcc aac ggc cct ctg ctt cgt tcc ctg tgc gcc cgc aac aat atc				739
Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys Ala Arg Asn Asn Ile				
	200	205	210	
gag gtc atc gcg gga ctg cac acc aac gac gat cct gaa cga ctc cgc				787
Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp Pro Glu Arg Leu Arg				
	215	220	225	
ttt gaa ctg gaa aac gcc att gac cag tat caa ccg gat gtc atc atc				835
Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln Pro Asp Val Ile Ile				
	230	235	240	245
acc tct ggc ggt atc agc cac ggt aaa ttt gag gtg ttt agg cag atc				883
Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu Val Phe Arg Gln Ile				
	250	255	260	
ctc gaa ggc acc ccg aac tcc tgg ttt gga cat gtc gat cag cag cct				931
Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His Val Asp Gln Gln Pro				
	265	270	275	
ggc ggt cct caa ggc atc tcc act ttt gct gaa act cct gtc att tca				979
Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu Thr Pro Val Ile Ser				
	280	285	290	
ctt ccc gga aat ccg att tcc acc ttg gtg agt ttc aca ctt ttg gtc				
1027				
Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser Phe Thr Leu Leu Val				
	295	300	305	
gcg cca gcg ctc aac cgc cag ccg ctc cgc cac ctc gat gcc cgc atc				
1075				
Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His Leu Asp Ala Arg Ile				
	310	315	320	325
acc gct ccg gtc cag ggc ttg caa gac aat cgc gag caa ttc ctt cgc				
1123				
Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg Glu Gln Phe Leu Arg				
	330	335	340	
ggc acc atc agt tac cgc aac ggg cca cgt cct cgc cac gcc tct cct				
1171				
Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro Arg His Ala Ser Pro				
	345	350	355	
ggg cac cag ttc cca cct gct ggt tca agc tgc cac cgc aga ctg tct				
1219				
Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys His Arg Arg Leu Ser				
	360	365	370	
gat cag gat ccc ggc gcg gac tac ggt gga gga aaa cga cat cgt				
1264				

Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly Lys Arg His Arg
 375 380 385

taagattttac ccattcaact aac
 1287

<210> 752

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 752

Met Ser Arg Ser Pro Glu Gln His Leu Ala Glu Ile Ser Ala Leu Leu
 1 5 10 15

Pro Pro Gln Lys Ser Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg
 20 25 30

Arg Thr Phe Ser Ala Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp
 35 40 45

Asn Ser Gln Met Asp Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly
 50 55 60

Gly Thr Phe Ala Val Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp
 65 70 75 80

Gln Trp Tyr Pro Arg Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr
 85 90 95

Gly Ala Arg Leu Pro Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys
 100 105 110

Thr Thr Pro Gly Asn Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr
 115 120 125

Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly
 130 135 140

Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly
 145 150 155 160

Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro
 165 170 175

Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly
 180 185 190

Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys
 195 200 205

Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp
 210 215 220

Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln
 225 230 235 240

Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu
 245 250 255

Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His
260 265 270

Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu
275 280 285

Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser
290 295 300

Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His
305 310 315 320

Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg
325 330 335

Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro
340 345 350

Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys
355 360 365

His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly
370 375 380

Lys Arg His Arg
385

<210> 753

<211> 815

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(792)

<223> FRXA00441

<400> 753

atc ccc gcc acc ccg caa ggt cag ttc ata cgg ttg cag ggt tcg gat 48
Ile Pro Ala Thr Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp
1 5 10 15

att act gcc ggc gac gag atc att cca gca ggt acg gag ctt aac tcg 96
Ile Thr Ala Gly Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser
20 25 30

gtg cac atc ggg gtg ttg gct agt cag tcg atc aag agc att gaa gtc 144
Val His Ile Gly Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val
35 40 45

gca gca aag cca cgt gtc ctc atc atc acc ggc ggg tct gaa att tca 192
Ala Ala Lys Pro Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser
50 55 60

gaa cag cac gga ccc gcc acg atc cct gat gcc aac ggc cct ctg ctt 240
Glu Gln His Gly Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu
65 70 75 80

cgt tcc ctg tgc gcc cgc aac aat atc gag gtc atc gcg gga ctg cac 288
Arg Ser Leu Cys Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His

85										90					95					
acc aac gac gat cct gaa cga ctc cgc ttt gaa ctg gaa aac gcc att	336																			
Thr Asn Asp Asp Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile																				
100 105 110																				
gac cag tat caa ccg gat gtc atc atc acc tct ggc ggt atc agc cac	384																			
Asp Gln Tyr Gln Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His																				
115 120 125																				
ggt aaa ttt gag gtg ttt agg cag atc ctc gaa ggc acc ccg aac tcc	432																			
Gly Lys Phe Glu Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser																				
130 135 140																				
tgg ttt gga cat gtc gat cag cag cct ggc ggt cct caa ggc atc tcc	480																			
Trp Phe Gly His Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser																				
145 150 155 160																				
act ttt gct gaa act cct gtc att tca ctt ccc gga aat ccg att tcc	528																			
Thr Phe Ala Glu Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser																				
165 170 175																				
acc ttg gtg agt ttc aca ctt ttg gtc gcg cca gcg ctc aac cgc cag	576																			
Thr Leu Val Ser Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln																				
180 185 190																				
ccg ctc cgc cac ctc gat gcc cgc atc acc gct ccg gtc cag ggc ttg	624																			
Pro Leu Arg His Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu																				
195 200 205																				
caa gac aat cgc gag caa ttc ctt cgc ggc acc atc agt tac cgc aac	672																			
Gln Asp Asn Arg Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn																				
210 215 220																				
ggg cca cgt cct cgc cac gcc tct cct ggg cac cag ttc cca cct gct	720																			
Gly Pro Arg Pro Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala																				
225 230 235 240																				
ggt tca agc tgc cac cgc aga ctg tct gat cag gat ccc ggc gcg gac	768																			
Gly Ser Ser Cys His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp																				
245 250 255																				
tac ggt gga gga aaa cga cat cgt taagatttac ccattcaact aac	815																			
Tyr Gly Gly Gly Lys Arg His Arg																				
260																				

<210> 754

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 754

Ile Pro Ala Thr Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp
 1 5 10 15

Ile Thr Ala Gly Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser
 20 25 30

Val His Ile Gly Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val
 35 40 45

Ala Ala Lys Pro Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser
 50 55 60

Glu Gln His Gly Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu
 65 70 75 80

Arg Ser Leu Cys Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His
 85 90 95

Thr Asn Asp Asp Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile
 100 105 110

Asp Gln Tyr Gln Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His
 115 120 125

Gly Lys Phe Glu Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser
 130 135 140

Trp Phe Gly His Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser
 145 150 155 160

Thr Phe Ala Glu Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser
 165 170 175

Thr Leu Val Ser Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln
 180 185 190

Pro Leu Arg His Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu
 195 200 205

Gln Asp Asn Arg Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn
 210 215 220

Gly Pro Arg Pro Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala
 225 230 235 240

Gly Ser Ser Cys His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp
 245 250 255

Tyr Gly Gly Gly Lys Arg His Arg
 260

<210> 755
 <211> 2358
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2335)
 <223> RXN02085

<400> 755
 caccggtga ttctgcgaac cttgaaacat cgtcagaaga ttgccgtgcg tcc tagccgg 60

gatccgcacg ttccggtcaa gcagaaagtc ttttaactcac atg act tcc aac ttt 115
 Met Thr Ser Asn Phe
 1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg	163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu	
10 15 20	
aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa	211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu	
25 30 35	
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg	259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu	
40 45 50	
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca	307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala	
55 60 65	
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat	355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp	
70 75 80 85	
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc	403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	
90 95 100	
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg	451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
105 110 115	
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct	499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
120 125 130	
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc	547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
135 140 145	
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt	595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
150 155 160 165	
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct	643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	
170 175 180	
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc	739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc	835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc	883

Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly
 250 255 260

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc
 1027
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac
 1075
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc
 1123
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta
 1171
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att
 1219
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc
 1267
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag
 1315
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
 390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc
 1363
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
 410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa
 1411
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat
 1459
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
 440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac
1507

Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
455 460 465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc
1555

Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
470 475 480 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc
1603

Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg
1651

Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag
1699

Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc
1747

His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca
1795

Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
550 555 560 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag
1843

Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
570 575 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccg cta cga
1891

Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg
585 590 595

gac gtc gat aag cct gcc tac ctg cag tgg tcc gtg gac tcc ttc cgc
1939

Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg
600 605 610

ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg
1987

Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met
615 620 625

tgc tac tcc gag ttc aac gaa gtg atc tcc tcg gtc atc gcg ttg gat
2035

Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp
630 635 640 645

gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc
2083

Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu
650 655 660

gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg
2131

Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val
665 670 675

tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt
2179

Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly
680 685 690

ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc
2227

Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val
695 700 705

aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct
2275

Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala
710 715 720 725

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc
2323

Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile
730 735 740

gga gca act atc taaattgggt taccgctagg aac
2358

Gly Ala Thr Ile
745

<210> 756

<211> 745

<212> PRT

<213> Corynebacterium glutamicum

<400> 756

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu

100	105	110
Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu 115	120	125
Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala 130	135	140
Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg 145	150	155
Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr 165	170	175
Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr 180	185	190
Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu 195	200	205
Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg 210	215	220
Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr 225	230	235
Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly 245	250	255
Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu 260	265	270
Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly 275	280	285
Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys 290	295	300
Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu 305	310	315
Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val 325	330	335
Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu 340	345	350
Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala 355	360	365
Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro 370	375	380
Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg 385	390	395
Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr 405	410	415
Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala 420	425	430

Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
 500 505 510
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
 530 535 540
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
 545 550 555 560
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
 565 570 575
 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
 580 585 590
 Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser
 595 600 605
 Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
 610 615 620
 Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser
 625 630 635 640
 Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
 645 650 655
 Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
 660 665 670
 Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala
 675 680 685
 Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro
 690 695 700
 Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp
 705 710 715 720
 Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln
 725 730 735
 Ala Arg Glu Lys Ile Gly Ala Thr Ile
 740 745

<400> 757																		
cacc	cggt	ga	tttc	gcga	ac	cttg	aaac	at	cgtc	aga	agt	gcc	gtg	cg	tct	agcc	cg	60
gatccgcacg ttcgggtcaa gcagaaagtc tttaactcac atg act tcc aac ttt																	115	
Met Thr Ser Asn Phe																		
1 5																		
tct	tcc	act	gtc	gct	ggt	ctt	cct	cg	atc	gga	gcg	aag	cgt	gaa	ctg			163
Ser	Ser	Thr	Val	Ala	Gly	Leu	Pro	Arg	Ile	Gly	Ala	Lys	Arg	Glu	Leu			
10 15 20																		
aag	ttc	gcg	ctc	gaa	ggc	tac	tgg	aat	gga	tca	att	gaa	ggt	cg	gaa			211
Lys	Phe	Ala	Leu	Glu	Gly	Tyr	Trp	Asn	Gly	Ser	Ile	Glu	Gly	Arg	Glu			
25 30 35																		
ctt	gcg	cag	acc	gcc	cg	caa	ttg	gtc	aac	act	gca	tcg	gat	tct	ttg			259
Leu	Ala	Gln	Thr	Ala	Arg	Gln	Leu	Val	Asn	Thr	Ala	Ser	Asp	Ser	Leu			
40 45 50																		
tct	gga	ttg	gat	tcc	gtt	ccg	ttt	gca	gga	cgt	tcc	tac	tac	gac	gca			307
Ser	Gly	Leu	Asp	Ser	Val	Pro	Phe	Ala	Gly	Arg	Ser	Tyr	Tyr	Asp	Ala			
55 60 65																		
atg	ctc	gat	acc	gcc	gct	att	ttg	ggt	gtg	ctg	ccg	gag	cgt	ttt	gat			355
Met	Leu	Asp	Thr	Ala	Ala	Ile	Leu	Gly	Val	Leu	Pro	Glu	Arg	Phe	Asp			
70 75 80 85																		
gac	atc	gct	gat	cat	gaa	aac	gat	ggt	ctc	cca	ctg	tgg	att	gac	cg			403
Asp	Ile	Ala	Asp	His	Glu	Asn	Asp	Gly	Leu	Pro	Leu	Trp	Ile	Asp	Arg			
90 95 100																		
tac	ttt	ggc	gct	gct	cg	ggt	act	gag	acc	ctg	cct	gca	cag	gca	atg			451
Tyr	Phe	Gly	Ala	Ala	Arg	Gly	Thr	Glu	Thr	Leu	Pro	Ala	Gln	Ala	Met			
105 110 115																		
acc	aag	tgg	ttt	gat	acc	aac	tac	cac	tac	ctc	gtg	ccg	gag	ttg	tct			499
Thr	Lys	Trp	Phe	Asp	Thr	Asn	Tyr	His	Tyr	Leu	Val	Pro	Glu	Leu	Ser			
120 125 130																		
gcg	gat	aca	cgt	ttc	gtt	ttg	gat	gcg	tcc	gcg	ctg	att	gag	gat	ctc			547
Ala	Asp	Thr	Arg	Phe	Val	Leu	Asp	Ala	Ser	Ala	Leu	Ile	Glu	Asp	Leu			
135 140 145																		
cgt	tgc	cag	cag	gtt	cgt	ggc	gtt	aat	gcc	cg	cct	gtt	ctg	gtt	ggt			595
Arg	Cys	Gln	Gln	Val	Arg	Gly	Val	Asn	Ala	Arg	Pro	Val	Leu	Val	Gly			
150 155 160 165																		
cca	ctg	act	ttc	ctt	tcc	ctt	gct	cg	acc	act	gat	ggt	tcc	aat	cct			643
Pro	Leu	Thr	Phe	Leu	Ser	Leu	Ala	Arg	Thr	Thr	Asp	Gly	Ser	Asn	Pro			
170 175 180																		

ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag 691
 Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys
 185 190 195

tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc 739
 Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr
 200 205 210

gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act 787
 Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr
 215 220 225

ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc 835
 Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly
 230 235 240 245

gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc 883
 Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly
 250 255 260

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc
 1027
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac
 1075
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc
 1123
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta
 1171
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att
 1219
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc
 1267
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag
 1315

Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc
1363

Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa
1411

Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat
1459

Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac
1507

Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
455 460 465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc
1555

Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
470 475 480 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc
1603

Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg
1651

Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag
1699

Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc
1747

His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca
1795

Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
550 555 560 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag
1843

Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
570 575 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg
1891

Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr

585

590

595

aga cgt cga taagcctgcc tacctgcagt ggt

1923

Arg Arg Arg

600

<210> 758

<211> 600

<212> PRT

<213> Corynebacterium glutamicum

<400> 758

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
1 5 10 15Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
20 25 30Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
50 55 60Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
65 70 75 80Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
85 90 95Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
100 105 110Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
115 120 125Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
130 135 140Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
145 150 155 160Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
165 170 175Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
180 185 190Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
195 200 205Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
210 215 220Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
225 230 235 240Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
245 250 255

Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
 355 360 365
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
 370 375 380
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
 405 410 415
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
 420 425 430
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
 500 505 510
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
 530 535 540
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
 545 550 555 560
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
 565 570 575

Leu Leu Pro Ala Thr Arg Arg Arg
595 600

```
<220>  
<221> CDS  
<222> (101)..(580)  
<223> FRXA02086
```

<400> 759																
gatgatcagc	cgctggctac	cactgctgac	caggttgcac	tggcactgcg	cgatgaaatt											60
aacgatatc	tcgaggctgg	cgcgaagatc	atccaggtgg	atg	agc	ctg	cga	ttc								115
				Met	Ser	Leu	Arg	Phe								
				1				5								
gtg	aac	tgt	tgc	ccg	cta	cga	gac	gtc	gat	aag	cct	gcc	tac	ctg	cag	163
Val	Asn	Cys	Cys	Pro	Leu	Arg	Asp	Val	Asp	Lys	Pro	Ala	Tyr	Leu	Gln	
			10						15					20		
tgg	tcc	gtg	gac	tcc	ttc	cgc	ctg	gcg	act	gcc	ggc	gca	ccc	gac	gac	211
Trp	Ser	Val	Asp	Ser	Phe	Arg	Leu	Ala	Thr	Ala	Gly	Ala	Pro	Asp	Asp	
			25					30					35			
gtc	caa	atc	cac	acc	cac	atg	tgc	tac	tcc	gag	ttc	aac	gaa	gtg	atc	259
Val	Gln	Ile	His	Thr	His	Met	Cys	Tyr	Ser	Glu	Phe	Asn	Glu	Val	Ile	
		40					45					50				
tcc	tcg	gtc	atc	gcg	ttg	gat	gcc	gat	gtc	acc	acc	atc	gaa	gca	gca	307
Ser	Ser	Val	Ile	Ala	Leu	Asp	Ala	Asp	Val	Thr	Thr	Ile	Glu	Ala	Ala	
		55				60					65					
cgt	tcc	gac	atg	cag	gtc	ctc	gct	gct	ctg	aaa	tct	tcc	ggc	ttc	gag	355
Arg	Ser	Asp	Met	Gln	Val	Leu	Ala	Ala	Leu	Lys	Ser	Ser	Gly	Phe	Glu	
		70				75				80					85	
ctc	ggc	gtc	gga	cct	ggg	gtg	tgg	gat	atc	cac	tcc	ccg	cgc	gtt	cct	403
Leu	Gly	Val	Gly	Pro	Gly	Val	Trp	Asp	Ile	His	Ser	Pro	Arg	Val	Pro	
				90					95					100		
tcc	gcg	cag	aaa	gtg	gac	ggg	ctc	ctc	gag	gct	gca	ctg	cag	tcc	gtg	451
Ser	Ala	Gln	Lys	Val	Asp	Gly	Leu	Leu	Glu	Ala	Ala	Leu	Gln	Ser	Val	
			105					110					115			
gat	cct	cgc	cag	ctg	tgg	gtc	aac	cca	gac	tgt	ggg	ctg	aag	acc	cgt	499
Asp	Pro	Arg	Gln	Leu	Trp	Val	Asn	Pro	Asp	Cys	Gly	Leu	Lys	Thr	Arg	
		120					125					130				
gga	tgg	cca	gaa	gtg	gaa	gct	tcc	cta	aag	gtt	ctc	gtt	gag	tcc	gct	547
Gly	Trp	Pro	Glu	Val	Glu	Ala	Ser	Leu	Lys	Val	Leu	Val	Glu	Ser	Ala	
		135				140					145					
aaq	caq	qct	cgt	gag	aaa	atc	gga	gca	act	atc	taaattgggt	taccgctagg				600

Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
150 155 160

aac

603

<210> 760
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 760
Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
1 5 10 15
Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
20 25 30
Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
35 40 45
Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
50 55 60
Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
65 70 75 80
Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
85 90 95
Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
100 105 110
Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
115 120 125
Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
130 135 140
Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
145 150 155 160

<210> 761
<211> 1326
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1303)
<223> RXN02648

<400> 761
atgaataaaa ttccgggtgc agtgaccgta ggtgaggtaa acgcggttag agtcgaatga 60
gagtttgata ctttctttcg accttttagat tggattttca atg agc cag aac cgc 115
Met Ser Gln Asn Arg

	1	5	
atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt			163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu			
	10	20	
gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc			211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe			
	25	35	
ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt			259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val			
	40	50	
gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc			307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr			
	55	65	
tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc			355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg			
	70	80	85
ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa			403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu			
	90	95	100
gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat			451
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp			
	105	110	115
cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct			499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser			
	120	125	130
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga			547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly			
	135	140	145
cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg			595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu			
	150	155	160
ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca			643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala			
	170	175	180
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac			691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp			
	185	190	195
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa			739
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu			
	200	205	210
tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca ccg			787
Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro			
	215	220	225
gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag			835
Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys			
	230	235	240
			245

gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca 883
 Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala
 250 255 260

gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc 931
 Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly
 265 270 275

tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att 979
 Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile
 280 285 290

ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca
 1027
 Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala
 295 300 305

tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt
 1075
 Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu
 310 315 320 325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tcc cac tcc atc aac
 1123
 Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn
 330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc
 1171
 Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
 345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg
 1219
 Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
 360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta
 1267
 Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
 375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac
 1313
 Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 390 395 400

aacgagggtt gct
 1326

<210> 762
 <211> 401
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 762
 Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220

Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240

Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255

Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270

His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285

Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300

Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320

Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335

Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg

340 345 350
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
 370 375 380
 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
 385 390 395 400
 Phe

<210> 763
 <211> 548
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(525)
 <223> FRXA02648

<400> 763
 gac gca ccg gac ttg gca gaa gca tgg gat cag atc aac cca gag cca 48
 Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
 1 5 10 15
 agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96
 Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30
 aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
 Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45
 tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60
 gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80
 gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95
 aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
 Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110
 tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384
 Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125
 cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160
 gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175
 taagctagac aacgagggtt gct 548

<210> 764

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 764

Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
 1 5 10 15
 Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30
 Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95
 Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110
 Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175

<210> 765

<211> 784

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(784)

<223> FRXA02658

<400> 765

atgaataaaa ttccgggtgc agtgaccgta ggtgaggtaa acgcgggttag agtcgaatga 60

gagtttgata cttttctttcg acttttagat tggattttca atg agc cag aac cgc 115
 Met Ser Gln Asn Arg
 1 5

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
 10 15 20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
 90 95 100

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
 105 110 115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 150 155 160 165

ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
 185 190 195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784

Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
 215 220 225

<210> 766

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 766

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220

Gln Leu Asp Ala
 225

<210> 767

<211> 513

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(490)

<223> RXA01516

<400> 767

tctgcacata tgggagcatg ggggtgtgcgc gtgcacgatg tcccagtatc aagggacgct 60

gttgatgttg ccgcattgtg gcgaagtgga ggaactcacc atg gct gat cgt att 115
Met Ala Asp Arg Ile
1 5

gaa ctt aaa ggc ctt gaa tgc ttc gga cac cac ggt gtg ttc gac ttt 163
Glu Leu Lys Gly Leu Glu Cys Phe Gly His His Gly Val Phe Asp Phe
10 15 20

gaa aaa gag caa ggc cag ccc ttc att gtg gat gtc acc tgc tgg atg 211
Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met
25 30 35

gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat 259
Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp
40 45 50

tac ggc gcg ttg gca ttg ttg gtt gct gaa atc gtg gaa ggc cca tcc 307
Tyr Gly Ala Leu Ala Leu Val Ala Glu Ile Val Glu Gly Pro Ser
55 60 65

agg gat ttg atc gag acg gtg gcc acg gaa tct gcg gat gct gtg atg 355
Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser Ala Asp Ala Val Met
70 75 80 85

gct aaa ttt gat gcg ctt cat gcg gtg gaa gta acc atc cat aag ccc 403
Ala Lys Phe Asp Ala Leu His Ala Val Glu Val Thr Ile His Lys Pro
90 95 100

aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gtt gcc cga 451
Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg
105 110 115

cgt tcc agg aaa tcc atg gct gct gga agg agc aac gcc taatgcatgc 500
Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser Asn Ala
120 125 130

agttttgtcc atc 513

<210> 768

<211> 130

<212> PRT

<213> Corynebacterium glutamicum

<400> 768

Met Ala Asp Arg Ile Glu Leu Lys Gly Leu Glu Cys Phe Gly His His
1 5 10 15

Gly Val Phe Asp Phe Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp
20 25 30

Val Thr Cys Trp Met Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu
35 40 45

Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile
50 55 60

Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser
65 70 75 80

Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val
85 90 95

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val
100 105 110

Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser
115 120 125

Asn Ala
130

<210> 769

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(952)

<223> RXA01515

<400> 769

taagcctggt gctgtgacca cgacgtctgc ggtgcgcggc gggtttaaga acaacgctgc 60

ctcccgcgct gaggtgttct cctgattcg ggggcactaa atg aac gta tcc tct 115
Met Asn Val Ser Ser
1 5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163
Leu Thr Ile Pro Gly Arg Cys Leu Val Ala Met Gly Ile Val Asn Val Thr
10 15 20

gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg 211
Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala
25 30 35

atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259
Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp
40 45 50

gtc ggc gcc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307
Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser
55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355
Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala
70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403
Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala
90 95 100

```

gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451
Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu
      105                      110                      115

gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499
Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val
      120                      125                      130

tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547
Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln
      135                      140                      145

gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595
Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp
      150                      155                      160                      165

gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643
Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile
      170                      175                      180

gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691
Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp
      185                      190                      195

cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739
Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile
      200                      205                      210

ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787
Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp
      215                      220                      225

cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835
Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala
      230                      235                      240                      245

gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883
Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His
      250                      255                      260

gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931
Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg
      265                      270                      275

```

```

agt gga gga act cac cat ggc tgatcgtatt gaacttaaag gcc 975
Ser Gly Gly Thr His His Gly
      280

```

<210> 770

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 770

```

Met Asn Val Ser Ser Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly
      1                      5                      10                      15

```

```

Ile Val Asn Val Thr Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile
      20                      25                      30

```

Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly
 35 40 45
 Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val
 50 55 60
 Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys
 65 70 75 80
 Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala
 85 90 95
 Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp
 100 105 110
 Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu
 115 120 125
 Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly
 130 135 140
 Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val
 145 150 155 160
 His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val
 165 170 175
 Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser
 180 185 190
 Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser
 195 200 205
 Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala
 210 215 220
 Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp
 225 230 235 240
 Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp
 245 250 255
 Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val
 260 265 270
 Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly
 275 280

<210> 771

<211> 859

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(859)

<223> RXA02024

<400> 771

cactgatgac ctggatcagg ccgtcaaatt catcgctgat gcacacgctg gattggacgt 60


```

agcgcgtctc cacaattaag cagtggctac attaggtgtt atg agt tct ttg ccg 115
Met Ser Ser Leu Pro
1 5

gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag 163
Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys
10 15 20

ggg gcg aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc 211
Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val
25 30 35

att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc 259
Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly
40 45 50

ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca 307
Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro
55 60 65

atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt 355
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val
70 75 80 85

gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca 403
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala
90 95 100

acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag 451
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln
105 110 115

gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg 499
Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly
120 125 130

gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg 547
Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val
135 140 145

gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt 595
Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg
150 155 160 165

gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc 643
Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe
170 175 180

ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag 691
Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu
185 190 195

gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat 739
Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp
200 205 210

ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc 787
Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly
215 220 225

```

acg ctt gct gcc act gcc tgg gcg gcg gcg cgc gcc gtt gcg gct ttt 835
 Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe
 230 235 240 245

cgc gtg cat gaa gtt gcg gaa acc 859
 Arg Val His Glu Val Ala Glu Thr
 250

<210> 772

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 772

Met Ser Ser Leu Pro Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp
 1 5 10 15

Ser Phe Tyr Asp Lys Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn
 20 25 30

Arg Ala Ala Glu Val Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly
 35 40 45

Gly Val Lys Ala Gly Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile
 50 55 60

Asp Arg Val Val Pro Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp
 65 70 75 80

Ile Asp Ile Ser Val Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala
 85 90 95

Val Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp
 100 105 110

His Glu Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys
 115 120 125

Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His
 130 135 140

Phe Asp Asp Ile Val Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala
 145 150 155 160

Glu Gln Ala Val Arg Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp
 165 170 175

Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu
 180 185 190

Arg Arg Ile Asp Glu Val Val Ala Thr Gly Trp Pro Val Leu Met Ala
 195 200 205

Leu Ser Asn Lys Asp Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp
 210 215 220

Lys Arg Val Ala Gly Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg
 225 230 235 240

Gly Val Ala Ala Phe Arg Val His Glu Val Ala Glu Thr

245

250

<210> 773
 <211> 684
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(661)
 <223> RXA01719

<400> 773
 ccatatgggc ggtgcactgg ctggaagtgg cggtattgca ctggtgactt cgtcgattgc 60
 cgaggacggg ctggttgatg ttgtgctggg gagaatgtaa atg aat atc atc att 115
 Met Asn Ile Ile Ile
 1 5
 ctt gct ggt ggc gag ggt aaa cgc atg ggt ggg gtg gat aag gct gct 163
 Leu Ala Gly Gly Glu Gly Lys Arg Met Gly Gly Val Asp Lys Ala Ala
 10 15 20
 gtg gcg gtg gat ggt cgc acg ctg ctg gat atc ctg ctt tca cag ctg 211
 Val Ala Val Asp Gly Arg Thr Leu Leu Asp Ile Leu Leu Ser Gln Leu
 25 30 35
 gat cca gaa gat gac gtc gtg gtg gtt tcc ccc gcg atc atc gac gga 259
 Asp Pro Glu Asp Asp Val Val Val Val Ser Pro Ala Ile Ile Asp Gly
 40 45 50
 atc acg act gtc tgc gag gaa cct ccg ctt ggc ggg ccg gtc gcg gga 307
 Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly Gly Pro Val Ala Gly
 55 60 65
 atc gag gca ggg ctg aat tct ttt gag cac gcc cat gaa ttc act gcg 355
 Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala His Glu Phe Thr Ala
 70 75 80 85
 att ctt gcc gtg gac gcg cct tat tct gca gcg atg ctg ccc cta ctt 403
 Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala Met Leu Pro Leu Leu
 90 95 100

cag gca cag att ggc aaa gcc gat gtg gcc gta acc ctt gct gcc gat 451
 Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val Thr Leu Ala Ala Asp
 105 110 115
 ggc tgg gta caa ccg ttg tgc gcg ctg tgg aga agt ggc agc cta gaa 499
 Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg Ser Gly Ser Leu Glu
 120 125 130
 gcg gtg att cac agc ctg ggc gag act aga aat cga ccg gca aaa gcg 547
 Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn Arg Pro Ala Lys Ala
 135 140 145
 tta ctg aag caa gcg gga cac att gtg gaa gtg ggt ggc gat ggc act 595
 Leu Leu Lys Gln Ala Gly His Ile Val Glu Val Gly Gly Asp Gly Thr
 150 155 160 165
 gaa aaa gac tac gat acg gtg gct gaa ctg gag gta ttg ggc aac gta 643

Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu Val Leu Gly Asn Val
 170 175 180

acg ctc cct aaa gcc cac tgatgagaaa cgtgagctct gct 684
 Thr Leu Pro Lys Ala His
 185

<210> 774

<211> 187

<212> PRT

<213> Corynebacterium glutamicum

<400> 774

Met Asn Ile Ile Ile Leu Ala Gly Gly Glu Gly Lys Arg Met Gly Gly
 1 5 10 15

Val Asp Lys Ala Ala Val Ala Val Asp Gly Arg Thr Leu Leu Asp Ile
 20 25 30

Leu Leu Ser Gln Leu Asp Pro Glu Asp Asp Val Val Val Val Ser Pro
 35 40 45

Ala Ile Ile Asp Gly Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly
 50 55 60

Gly Pro Val Ala Gly Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala
 65 70 75 80

His Glu Phe Thr Ala Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala
 85 90 95

Met Leu Pro Leu Leu Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val
 100 105 110

Thr Leu Ala Ala Asp Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg
 115 120 125

Ser Gly Ser Leu Glu Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn
 130 135 140

Arg Pro Ala Lys Ala Leu Leu Lys Gln Ala Gly His Ile Val Glu Val
 145 150 155 160

Gly Gly Asp Gly Thr Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu
 165 170 175

Val Leu Gly Asn Val Thr Leu Pro Lys Ala His
 180 185

<210> 775

<211> 1332

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1309)

<223> RXA01720

<400> 775

```

acacccggttt gagaatctca acctcttaaa acagcgcgaa ctattgattt ggcaactacc 60

ctatatattt gagtgtttat tgtcgaaaaa ggggttttcaa gtg gca cag caa cgc 115
                               Val Ala Gln Gln Arg
                               1                               5

agc gtc gat gac tat ctt tcc att ttg ata gac agc gtc gca ccg ctt 163
Ser Val Asp Asp Tyr Leu Ser Ile Leu Ile Asp Ser Val Ala Pro Leu
                               10                               15                               20

ccg cca gta aaa acc cct atc ctc ggc gcg cat ccg tta agt cac ctt 211
Pro Pro Val Lys Thr Pro Ile Leu Gly Ala His Pro Leu Ser His Leu
                               25                               30                               35

gca gag gat gtt gtc gcg aca att cct atc ccg aaa ttt act aat tct 259
Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro Lys Phe Thr Asn Ser
                               40                               45                               50

gct gtt gat ggt tac gcc att ttg aaa gaa gac atc cat ggc agc ggg 307
Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp Ile His Gly Ser Gly
                               55                               60                               65

ccg tgg aca ttt ctt gtg ggc ggt gat act ccg gcg ggt tct gcg ccg 355
Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro Ala Gly Ser Ala Pro
                               70                               75                               80                               85

gcg agc att aat aat gga aaa gcc atc cgt gtg atg aca ggt gga ccc 403
Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val Met Thr Gly Gly Pro
                               90                               95                               100

gtc cca tcc acc aac aag gac atg atc gtg gtt cca gtg gag ctc acc 451
Val Pro Ser Thr Asn Lys Asp Met Ile Val Val Pro Val Glu Leu Thr
                               105                               110                               115

aat gct ccg gtg gat cac tcg ctt cct aca gaa atc acg atc aat gag 499
Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu Ile Thr Ile Asn Glu
                               120                               125                               130

cta cca ggt gag agg aat aat att cgc cat gct ggt gag cat ctt aaa 547
Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala Gly Glu His Leu Lys
                               135                               140                               145

gaa ggc gaa att gcg gtt gct gcg ggg acg gca ttt gat gcg ggt act 595
Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala Phe Asp Ala Gly Thr
150                               155                               160                               165

gtg tcg acg gtg att tca gtt ggc cat gac act gta aaa gcc cat cct 643
Val Ser Thr Val Ile Ser Val Gly His Asp Thr Val Lys Ala His Pro
                               170                               175                               180

tgc cct cgg gtt gcg gtg atc act acc ggt gat gag cta aac cag gga 691
Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp Glu Leu Asn Gln Gly
                               185                               190                               195

aat ccc tgg ggt atc cct aat tcc aat ggg ccg atg ctg gtt gcg gag 739
Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro Met Leu Val Ala Glu
                               200                               205                               210

cta aaa cgc gtg ggg att aag gat ccg cag cat ttc cat tcc gat gat 787
Leu Lys Arg Val Gly Ile Lys Asp Pro Gln His Phe His Ser Asp Asp

```

215	220	225	
tct gag act gca ttg agg gag acg ctc gat aag cct gca gag gtt gcg			835
Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys Pro Ala Glu Val Ala			
230	235	240	245
gat gtg atc atc act gtg ggt ggg atc tcg gcg ggc gcg ttc gat gtg			883
Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala Gly Ala Phe Asp Val			
250	255		260
gtc aaa gcc gtg gga act aag act ggt ggt ttt gaa ttc ttc ccc att			931
Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe Glu Phe Phe Pro Ile			
265	270		275
gcg atg aag ccg ggt aaa ccg caa ggt cat ggg cag tgg ggc gac gca			979
Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly Gln Trp Gly Asp Ala			
280	285		290
aaa gtg gtg tgt ctg ccg gga aac ccg gtg gcg gcg tgg gtt agt ttt			
1027			
Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala Ala Trp Val Ser Phe			
295	300		305
agg ctc ttt gtt gtt ccg gta att gag aga tta ggg ggt gga aag agg			
1075			
Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu Gly Gly Gly Lys Arg			
310	315		320
ctg gcg tcg ata agc gaa ctc cct gtg gtg gcg ctg cgc tcg aac ccg			
1123			
Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala Leu Arg Ser Asn Arg			
330	335		340
gcg ctg aag gcg ccg gag ggc ccc gta ttg gcg ata ccg gtg gcg att			
1171			
Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala Ile Pro Val Ala Ile			
345	350		355
gat tgg gag aaa aga atg gca aat tct cag gca cat cga tcc cat atg			
1219			
Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala His Arg Ser His Met			
360	365		370
gtc ggt gca ctg gct gga agt ggc ggt att gca ctg gtg act tcg tcg			
1267			
Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala Leu Val Thr Ser Ser			
375	380		385
att gcc gag gac ggt ctg gtt gat gtt gtg ctg ggg aga atg			
1309			
Ile Ala Glu Asp Gly Leu Val Asp Val Val Leu Gly Arg Met			
390	395		400
taaatgaata tcatcattct tgc			
1332			

<210> 776

<211> 403

<212> PRT

<213> Corynebacterium glutamicum

<400> 776

Val Ala Gln Gln Arg Ser Val Asp Asp Tyr Leu Ser Ile Leu Ile Asp
1 5 10 15

Ser Val Ala Pro Leu Pro Pro Val Lys Thr Pro Ile Leu Gly Ala His
20 25 30

Pro Leu Ser His Leu Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro
35 40 45

Lys Phe Thr Asn Ser Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp
50 55 60

Ile His Gly Ser Gly Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro
65 70 75 80

Ala Gly Ser Ala Pro Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val
85 90 95

Met Thr Gly Gly Pro Val Pro Ser Thr Asn Lys Asp Met Ile Val Val
100 105 110

Pro Val Glu Leu Thr Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu
115 120 125

Ile Thr Ile Asn Glu Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala
130 135 140

Gly Glu His Leu Lys Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala
145 150 155 160

Phe Asp Ala Gly Thr Val Ser Thr Val Ile Ser Val Gly His Asp Thr
165 170 175

Val Lys Ala His Pro Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp
180 185 190

Glu Leu Asn Gln Gly Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro
195 200 205

Met Leu Val Ala Glu Leu Lys Arg Val Gly Ile Lys Asp Pro Gln His
210 215 220

Phe His Ser Asp Asp Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys
225 230 235 240

Pro Ala Glu Val Ala Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala
245 250 255

Gly Ala Phe Asp Val Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe
260 265 270

Glu Phe Phe Pro Ile Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly
275 280 285

Gln Trp Gly Asp Ala Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala
290 295 300

Ala Trp Val Ser Phe Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu
305 310 315 320

Gly Gly Gly Lys Arg Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala
 325 330 335

Leu Arg Ser Asn Arg Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala
 340 345 350

Ile Pro Val Ala Ile Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala
 355 360 365

His Arg Ser His Met Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala
 370 375 380

Leu Val Thr Ser Ser Ile Ala Glu Asp Gly Leu Val Asp Val Val Leu
 385 390 395 400

Gly Arg Met

<210> 777
 <211> 1237
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (2)..(1207)
 <223> RXS03223

<400> 777
 tcca gag cca gtg cgt att gct att gca gag gca ctg ggt ttg atg tgc 49
 Pro Glu Pro Val Arg Ile Ala Ile Ala Glu Ala Leu Gly Leu Met Cys
 1 5 10 15

gcg gaa gag gtt caa gct agt cgt gct ttg ccg ggt ttc gcg caa gca 97
 Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala
 20 25 30

gcg att gat ggt tat gcg gtt cga gca gtc gat gtc gcc gcc gag aag 145
 Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys
 35 40 45

tcg ttt agc cag caa ctg ccg gtt gct cct ccg gaa aaa tcc ctg ccc 193
 Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro
 50 55 60

gtg gtg ggt gaa gta gct gcg ggt tct cag cag ccg ttg cgc ctg cag 241
 Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln
 65 70 75 80

cct aaa caa gca gtc atg gtc cac acc ggt gcg cca ctg ccg atg ctt 289
 Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu
 85 90 95

gcg gat gcg gtg ctg ccc atg gcg tgg tca gat cgt gcc cgc aaa cga 337
 Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg
 100 105 110

gta acc gcg cag cga cct gtg cgc tct gcc gag ttt gtg cgc aaa gaa 385
 Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu

115	120	125	
ggc gat gac atc caa ccg gga gac atc gca gtc agc gcc ggc gcg gtc Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val 130 135 140			433
tta ggc cct gcc caa att ggt ttg ctc gca gct gtt ggt cgc tcc aaa Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys 145 150 155 160			481
gtg ttg gtg tac cca cgc cca cgc atg tcg gtt atc tcc gta ggc gct Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala 165 170 175			529
gaa ctt gtt gat att gat cgc cag cca ggc ctc ggc cag gtt tat gat Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp 180 185 190			577
gtc aat tcc tat tct ctg gct gcc gcc ggt agg gaa gcg ggc gca gat Val Asn Ser Tyr Ser Leu Ala Ala Gly Arg Glu Ala Gly Ala Asp 195 200 205			625
gtg tac cgc tac ggc att gct gcc ggt gaa cct cgt cgc atc aaa gag Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu 210 215 220			673
atc att gaa tcc cag atg ctg cgc tcg gaa atc atc gtc atc acc gga Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly 225 230 235 240			721
gct gtt ggc ggt gct ggt tca gct ggc gtg cgc cag gtt ctc aac gag Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu 245 250 255			769
cta ggc gat atc gac acc gaa cgc gtc gca atg cac ccc ggt tct gtc Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val 260 265 270			817
caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu 275 280 285			865
cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg 290 295 300			913
ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val 305 310 315 320			961
gtt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa 1009 Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys 325 330 335			
ggt ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac 1057 Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr 340 345 350			

ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg
 1105
 Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu
 355 360 365

gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc
 1153
 Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val
 370 375 380

aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa
 1201
 Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln
 385 390 395 400

ggt cga tagttcgatg cgtaatgcac cgtcaggtcc
 1237
 Gly Arg

<210> 778
 <211> 402
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 778
 Pro Glu Pro Val Arg Ile Ala Ile Ala Glu Ala Leu Gly Leu Met Cys
 1 5 10 15

Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala
 20 25 30

Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys
 35 40 45

Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro
 50 55 60

Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln
 65 70 75 80

Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu
 85 90 95

Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg
 100 105 110

Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu
 115 120 125

Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val
 130 135 140

Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys
 145 150 155 160

Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala
 165 170 175

Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp

180	185	190
Val Asn Ser Tyr Ser Leu Ala Ala Ala Gly Arg Glu Ala Gly Ala Asp 195 200 205		
Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu 210 215 220		
Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly 225 230 235 240		
Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu 245 250 255		
Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val 260 265 270		
Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu 275 280 285		
Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg 290 295 300		
Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val 305 310 315 320		
Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys 325 330 335		
Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr 340 345 350		
Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu 355 360 365		
Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val 370 375 380		
Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln 385 390 395 400		
Gly Arg		

<210> 779
 <211> 1229
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1) .. (1206)
 <223> FRXA01970

<400> 779
 cca gag cca gtg cgt att gct att gca gag gca ctg ggt ttg atg tgc 48
 Pro Glu Pro Val Arg Ile Ala Ile Ala Glu Ala Leu Gly Leu Met Cys
 1 5 10 15
 gcg gaa gag gtt caa gct agt cgt gct ttg ccg ggt ttc gcg caa gca 96

Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala	
20 25 30	
gcg att gat ggt tat gcg gtt cga gca gtc gat gtc ggc ggc gag aag	144
Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys	
35 40 45	
tcg ttt agc cag caa ctg ccg gtt gct cct ccg gaa aaa tcc ctg ccc	192
Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro	
50 55 60	
gtg gtg ggt gaa gta gct gcg ggt tct cag cag ccg ttg cgc ctg cag	240
Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln	
65 70 75 80	
cct aaa caa gca gtc atg gtc cac acc ggt gcg cca ctg ccg atg ctt	288
Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu	
85 90 95	
gcg gat gcg gtg ctg ccc atg gcg tgg tca gat cgt ggc cgc aaa cga	336
Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg	
100 105 110	
gta acc gcg cag cga cct gtg cgc tct ggc gag ttt gtg cgc aaa gaa	384
Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu	
115 120 125	
ggc gat gac atc caa ccg gga gac atc gca gtc agc gcc ggc gcg gtc	432
Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val	
130 135 140	
tta ggc cct gcc caa att ggt ttg ctg gca gct gtt ggt cgc tcc aaa	480
Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys	
145 150 155 160	
gtg ttg gtg tac cca cgc cca cgc atg tcg gtt atc tcc gta ggc gct	528
Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala	
165 170 175	
gaa ctt gtt gat att gat cgc cag cca ggc ctc ggc cag gtt tat gat	576
Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp	
180 185 190	
gtc aat tcc tat tct ctg gct gcc gcc ggt agg gaa gcg ggc gca gat	624
Val Asn Ser Tyr Ser Leu Ala Ala Ala Gly Arg Glu Ala Gly Ala Asp	
195 200 205	
gtg tac cgc tac ggc att gct gcc ggt gaa cct cgt cgc atc aaa gag	672
Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu	
210 215 220	
atc att gaa tcc cag atg ctg cgc tcg gaa atc atc gtc atc acc gga	720
Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly	
225 230 235 240	
gct gtt ggc ggt gct ggt tca gct gcc gtg cgc cag gtt ctc aac gag	768
Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu	
245 250 255	
cta ggc gat atc gac acc gaa cgc gtc gca atg cac ccc ggt tct gtc	816
Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val	

260 265 270
 caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg 864
 Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu
 275 280 285
 cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc 912
 Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg
 290 295 300
 ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt 960
 Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val
 305 310 315 320
 gtt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa
 1008
 Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys
 325 330 335
 ggt ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac
 1056
 Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr
 340 345 350
 ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg
 1104
 Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu
 355 360 365
 gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc
 1152
 Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val
 370 375 380
 aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa
 1200
 Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln
 385 390 395 400
 ggt cga tagttcgatg cgtaatgcac cgt
 1229
 Gly Arg

<210> 780

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 780

Pro Glu Pro Val Arg Ile Ala Ile Ala Glu Ala Leu Gly Leu Met Cys
 1 5 10 15
 Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala
 20 25 30
 Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys
 35 40 45
 Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro

50	55	60
Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln		
65	70	75 80
Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu		
	85	90 95
Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg		
	100	105 110
Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu		
	115	120 125
Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val		
	130	135 140
Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys		
	145	150 155 160
Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala		
	165	170 175
Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp		
	180	185 190
Val Asn Ser Tyr Ser Leu Ala Ala Gly Arg Glu Ala Gly Ala Asp		
	195	200 205
Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu		
	210	215 220
Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly		
	225	230 235 240
Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu		
	245	250 255
Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val		
	260	265 270
Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu		
	275	280 285
Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg		
	290	295 300
Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val		
	305	310 315 320
Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys		
	325	330 335
Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr		
	340	345 350
Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu		
	355	360 365
Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val		
	370	375 380

Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln
 385 390 395 400

Gly Arg

<210> 781

<211> 708

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(685)

<223> RXA02629

<400> 781

tacctcgcag agccgggagg tagagggttac tctgacgagt gagtaggttt aaaagagtta 60

atctgcatct aatcaagtag ccaagtatga gtgaggaaca atg agc aag gat cca 115
 Met Ser Lys Asp Pro
 1 5

ttg gga agt ctt acc gat gtt gta gac aca cga gtt ccg ctt ccg gat 163
 Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg Val Pro Leu Pro Asp
 10 15 20

gtt gaa ccg gat ccg gag ttc ctg aag gct acg gaa aaa gaa ttc cac 211
 Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr Glu Lys Glu Phe His
 25 30 35

atg gca tcc cag aag cgc gct ctt gtt gtc ctg gtg ggc gat cat gtc 259
 Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu Val Gly Asp His Val
 40 45 50

gct gag gca gat ggg act ggc cgt ttg gtt acg gag ctg ctc tta gag 307
 Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr Glu Leu Leu Leu Glu
 55 60 65

tct ggc ttc aac gtg gac gct gtg gtc agc gtg aag tct aag aag tct 355
 Ser Gly Phe Asn Val Asp Ala Val Val Ser Val Lys Ser Lys Lys Ser
 70 75 80 85

cag att agg caa gct att gaa acc gca gtt gtt ggc ggc gct gac ctt 403
 Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val Gly Gly Ala Asp Leu
 90 95 100

gtg ctg acc atc ggc gga gtg ggc gtt ggt cct cgg gat aaa act cct 451
 Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro Arg Asp Lys Thr Pro
 105 110 115

gag gca acc agc gct gtg ttg gac cag gac gtc cca gga atc gcg cag 499
 Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val Pro Gly Ile Ala Gln
 120 125 130

gcg ctt cgt tcc tcc ggt ttg gcc tgt ggc gcg gtg gat gca agt gtt 547
 Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala Val Asp Ala Ser Val
 135 140 145

tcc cga ggc gta gcg ggc gta tcc ggc tca acc gtg gtg gtc aac ctc 595
 Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr Val Val Val Asn Leu
 150 155 160 165

gct gag tct cgt tcg gca att cgt gat ggc atg gca act ctg aca ccg 643
 Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met Ala Thr Leu Thr Pro
 170 175 180

ttg gtt gat ttt gtt gta gat cag ctt cgc act tcc gtg gtt 685
 Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr Ser Val Val
 185 190 195

tgagttgggc ggggtgtgagt aga 708

<210> 782

<211> 195

<212> PRT

<213> Corynebacterium glutamicum

<400> 782

Met Ser Lys Asp Pro Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg
 1 5 10 15

Val Pro Leu Pro Asp Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr
 20 25 30

Glu Lys Glu Phe His Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu
 35 40 45

Val Gly Asp His Val Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr
 50 55 60

Glu Leu Leu Leu Glu Ser Gly Phe Asn Val Asp Ala Val Val Ser Val
 65 70 75 80

Lys Ser Lys Lys Ser Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val
 85 90 95

Gly Gly Ala Asp Leu Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro
 100 105 110

Arg Asp Lys Thr Pro Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val
 115 120 125

Pro Gly Ile Ala Gln Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala
 130 135 140

Val Asp Ala Ser Val Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr
 145 150 155 160

Val Val Val Asn Leu Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met
 165 170 175

Ala Thr Leu Thr Pro Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr
 180 185 190

Ser Val Val
 195


```
<220>  
<221> CDS  
<222> (101)..(379)  
<223> RXA02318
```

```

<400> 783
gatatacgcc acggtaccgc gtacaaaatc ccgaatatga tcatggccaa aggaggtcag 60

cagtaagcgc atgtgcgcca ttttaaggca agatggggcc atg aat tcg ctt ttc 115
Met Asn Ser Leu Phe
1 5

gac gtc tcc cca cac tgg tcc tcc gcc aac gcc aag ctc acc gca cat 163
Asp Val Ser Pro His Trp Ser Ser Ala Asn Ala Lys Leu Thr Ala His
10 15 20

ttt aac acc gga aaa ttc tcc act ggc atg aaa ttt gtc aac ctc att 211
Phe Asn Thr Gly Lys Phe Ser Thr Gly Met Lys Phe Val Asn Leu Ile
25 30 35

gcc gac tcc gca gaa gaa gcc aac cac cac ccc gat atc ctt ctc acc 259
Ala Asp Ser Ala Glu Glu Ala Asn His His Pro Asp Ile Leu Leu Thr
40 45 50

tat ggt ttt gtg gaa atc acc ctc acc agc cac gat gtg ggt gag ata 307
Tyr Gly Phe Val Glu Ile Thr Leu Thr Ser His Asp Val Gly Glu Ile
55 60 65

acc gac cgt gat gtc gcc cta gca aaa gtc atc gac gcc cac gcc aag 355
Thr Asp Arg Asp Val Ala Leu Ala Lys Val Ile Asp Ala His Ala Lys
70 75 80 85

acc ttg gcc att tcg gca gag gct taagggttaaa gattatgagc aac 402
Thr Leu Ala Ile Ser Ala Glu Ala
90

```

```

<400> 784
Met Asn Ser Leu Phe Asp Val Ser Pro His Trp Ser Ser Ala Asn Ala
  1             5             10             15

Lys Leu Thr Ala His Phe Asn Thr Gly Lys Phe Ser Thr Gly Met Lys
          20             25             30

Phe Val Asn Leu Ile Ala Asp Ser Ala Glu Glu Ala Asn His His Pro
          35             40             45

Asp Ile Leu Leu Thr Tyr Gly Phe Val Glu Ile Thr Leu Thr Ser His
  50             55             60

Asp Val Gly Glu Ile Thr Asp Arg Asp Val Ala Leu Ala Lys Val Ile

```


150

155

gca

600

<210> 786

<211> 159

<212> PRT

<213> Corynebacterium glutamicum

<400> 786

Met His Ala Val Leu Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala
 1 5 10 15

Leu Leu Asn Thr Val Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln
 20 25 30

Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu
 35 40 45

Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu
 50 55 60

Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg
 65 70 75 80

Val Arg Lys Trp Gly Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile
 85 90 95

Ile Lys Asp Gly Glu Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu
 100 105 110

Pro His Pro Trp Ala Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu
 115 120 125

Glu Ala Glu Pro Asp Ala Val Leu His Gly Thr Thr Ile Ala Glu His
 130 135 140

Val Asp Asn Leu Asp Pro Thr Asp Ile Glu Gly Val Thr Lys Ile
 145 150 155

<210> 787

<211> 609

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(586)

<223> RXN01304

<400> 787

atgcaggtaa acgaatttgt gcttatatca acattcgtga ttccggcaaaa ttaattaaac 60

tgaaaaaggg gattaattac cccacttga ggagaaattg atg ccc gca cag aac 115
 Met Pro Ala Gln Asn
 1 5

aaa aac ctc cca gga tcc gtc atc gtt gtg tct gat cgg att aaa tcg 163
 Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser Asp Arg Ile Lys Ser

	10	15	20	
gga gaa aga att gat aaa gca gga ccc gta gca gta gac ctt ctt cag				211
Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala Val Asp Leu Leu Gln				
	25	30	35	
gaa tca ggc gtg gag att tcc aca ttc acc gtc gtg gag gag ggc ttt				259
Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val Val Glu Glu Gly Phe				
	40	45	50	
gaa cct gtc cat caa gaa ttg gtt aag gcg ttg gcg cgc cgg gat cgc				307
Glu Pro Val His Gln Glu Leu Val Lys Ala Leu Ala Arg Arg Asp Arg				
	55	60	65	
gtc atc atc acc atc ggc gga acg ggc gtg ggg cct aga aat cgg acg				355
Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly Pro Arg Asn Arg Thr				
	70	75	80	85
ccg gag gcc aca gaa ccg cac atc gat acg cta ctg ccg ggt ctg atg				403
Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu Leu Pro Gly Leu Met				
	90	95	100	
acg cag att ttg ttc tct gga ctg tcc aat acc gcg cag gcg ggg tta				451
Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr Ala Gln Ala Gly Leu				
	105	110	115	
tct cgg ggg ctg gtg ggc ttg agt gct cgc gat tcc acg gcc gcg ctc				499
Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp Ser Thr Ala Ala Leu				
	120	125	130	
atc gtc aac gcg ccg agt tct tcc ggg ggc gtg cgc gac gcg ctc ggg				547
Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val Arg Asp Ala Leu Gly				
	135	140	145	
gtg gtc tgc ccg ctt ttc ggt tcc att ttt gag cgt ctt taaaagattt				596
Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu Arg Leu				
	150	155	160	
ttgcttatcg acg				609

<210> 788

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 788

Met	Pro	Ala	Gln	Asn	Lys	Asn	Leu	Pro	Gly	Ser	Val	Ile	Val	Val	Ser
1				5					10					15	

Asp	Arg	Ile	Lys	Ser	Gly	Glu	Arg	Ile	Asp	Lys	Ala	Gly	Pro	Val	Ala
		20						25					30		

Val	Asp	Leu	Leu	Gln	Glu	Ser	Gly	Val	Glu	Ile	Ser	Thr	Phe	Thr	Val
		35					40					45			

Val	Glu	Glu	Gly	Phe	Glu	Pro	Val	His	Gln	Glu	Leu	Val	Lys	Ala	Leu
	50						55						60		

Ala	Arg	Arg	Asp	Arg	Val	Ile	Ile	Thr	Ile	Gly	Gly	Thr	Gly	Val	Gly
	65					70				75					80

<400> 789																		
tgccatcata	ttaaggccaa	attgcttga	tcctgggatt	tatttaatta	gattaaatcc													60
gtagaaatta gcccatgaag catggaaagg cgaaaacccc																		115
				ttg	atc	gtt	tcc	acc										
				Leu	Ile	Val	Ser	Thr										
				1				5										
cag	ccc	att	act	gat	cgc	agc	gca	ctc	tcg	gca	gaa	cac	gca	gag	gtg	163		
Gln	Pro	Ile	Thr	Asp	Arg	Ser	Ala	Leu	Ser	Ala	Glu	His	Ala	Glu	Val			
				10				15					20					
atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg																		211
Ile	Lys	Ala	Thr	Leu	Pro	Leu	Val	Gly	Gly	Lys	Ile	Asn	Glu	Ile	Thr			
			25				30					35						
ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct																		259
Pro	Val	Phe	Tyr	Asn	Lys	Met	Phe	Ala	Ala	His	Pro	Glu	Leu	Ile	Ala			
			40				45					50						
aac acc ttc aac cgt ggc aat cag aag caa ggc gat cag cag aag gcg																		307
Asn	Thr	Phe	Asn	Arg	Gly	Asn	Gln	Lys	Gln	Gly	Asp	Gln	Gln	Lys	Ala			
			55			60					65							
ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat																		355
Leu	Ala	Ala	Ser	Ile	Ala	Thr	Phe	Ala	Thr	Met	Leu	Val	Thr	Pro	Asp			
			70			75				80					85			
gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg																		403
Ala	Pro	Asp	Pro	Val	Gln	Leu	Ile	Ser	Arg	Ile	Gly	His	Lys	His	Val			
				90				95					100					

tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg 451
 Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu
 105 110 115

ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct 499
 Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro
 120 125 130

gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg 547
 Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu
 135 140 145

atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc 595
 Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly
 150 155 160 165

gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca 643
 Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala
 170 175 180

acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca 691
 Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro
 185 190 195

ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag 739
 Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln
 200 205 210

ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att 787
 Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile
 215 220 225

gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta 835
 Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val
 230 235 240 245

tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt 883
 Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val
 250 255 260

ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc 931
 Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly
 265 270 275

tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac 979
 Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp
 280 285 290

gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg
 1027
 Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val
 295 300 305

gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa
 1075
 Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu
 310 315 320 325

atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att
 1123
 Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile

330 335 340
 cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag
 1171
 Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys
 345 350 355
 aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta
 1219
 Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val
 360 365 370
 aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca
 1268
 Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser
 375 380 385
 ccccgagaact tcc
 1281

<210> 790
 <211> 386
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 790
 Leu Ile Val Ser Thr Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala
 1 5 10 15
 Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys
 20 25 30
 Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His
 35 40 45
 Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly
 50 55 60
 Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met
 65 70 75 80
 Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile
 85 90 95

Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile
 100 105 110
 Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
 115 120 125
 Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile
 130 135 140
 Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn
 145 150 155 160
 Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
 165 170 175
 Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu

180	185	190
Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp		
195	200	205
Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp		
210	215	220
Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe		
225	230	235 240
Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala		
245	250	255
Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile		
260	265	270
Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met		
275	280	285
Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser		
290	295	300
Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro		
305	310	315 320
Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu		
325	330	335
Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly		
340	345	350
Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu		
355	360	365
Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu		
370	375	380
Ile Ser		
385		

<210> 791

<211> 990

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(967)

<223> RXS02560

<400> 791

ttgggggcaag ccagctaacg catttcttgt ggaaaccgca gacattgagg ccgcccacgc 60

ggaacttcta agagcagtgg aatgaaataa tccggtgctg atg cag ggc aac tcg	115
Met Gln Gly Asn Ser	
1 5	

ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca	163
Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro	

10								15				20				
gga	gaa	ctt	tta	gcc	gcc	cgc	tac	gga	caa	cct	gca	acc	tgg	acg	cca	211
Gly	Glu	Leu	Leu	Ala	Ala	Arg	Tyr	Gly	Gln	Pro	Ala	Thr	Trp	Thr	Pro	
		25						30					35			
ccg	cag	tgg	aat	gag	acg	ctt	gat	gtc	att	cac	cag	cat	cga	tca	gtt	259
Pro	Gln	Trp	Asn	Glu	Thr	Leu	Asp	Val	Ile	His	Gln	His	Arg	Ser	Val	
		40					45					50				
cgc	agg	tgg	ttg	gat	aaa	ccg	gtt	gat	gat	gac	acc	atc	cgc	acc	att	307
Arg	Arg	Trp	Leu	Asp	Lys	Pro	Val	Asp	Asp	Asp	Thr	Ile	Arg	Thr	Ile	
		55				60					65					
att	tcc	gcc	gca	caa	tcg	gct	gga	acc	tct	tcc	aat	aag	cag	gtc	att	355
Ile	Ser	Ala	Ala	Gln	Ser	Ala	Gly	Thr	Ser	Ser	Asn	Lys	Gln	Val	Ile	
	70				75					80					85	
tct	gtc	atc	gtg	gtt	aaa	gat	cct	gag	ctg	agg	aaa	ggc	ctc	gcg	ggg	403
Ser	Val	Ile	Val	Val	Lys	Asp	Pro	Glu	Leu	Arg	Lys	Gly	Leu	Ala	Gly	
			90					95					100			
atc	act	cgc	cag	atg	ttt	ccg	cac	ctt	gag	cag	gtt	ccc	gcg	gtg	ctg	451
Ile	Thr	Arg	Gln	Met	Phe	Pro	His	Leu	Glu	Gln	Val	Pro	Ala	Val	Leu	
			105					110					115			
att	tgg	ttg	att	gat	tat	tcc	cga	atc	agt	gcg	gtg	gca	gcc	aga	gaa	499
Ile	Trp	Leu	Ile	Asp	Tyr	Ser	Arg	Ile	Ser	Ala	Val	Ala	Ala	Arg	Glu	
		120					125					130				
gat	ctc	cca	aca	ggg	gct	ctt	gat	tat	ctc	gat	gag	gcc	gcg	tgg	ggg	547
Asp	Leu	Pro	Thr	Gly	Ala	Leu	Asp	Tyr	Leu	Asp	Glu	Ala	Ala	Trp	Gly	
	135					140					145					
ttc	ctc	gac	gcc	gga	atc	gca	gct	caa	aac	gct	gca	att	gct	gcg	gag	595
Phe	Leu	Asp	Ala	Gly	Ile	Ala	Ala	Gln	Asn	Ala	Ala	Ile	Ala	Ala	Glu	
	150				155				160						165	
tca	ctt	gga	ttg	gga	acg	ctc	tat	ttg	ggt	tcg	gtg	cgc	aac	gat	gcg	643
Ser	Leu	Gly	Leu	Gly	Thr	Leu	Tyr	Leu	Gly	Ser	Val	Arg	Asn	Asp	Ala	
			170					175					180			
gaa	gcc	gtg	cac	aaa	ttg	ctt	ggc	ctt	cca	cct	gag	atc	gtg	cct	gtc	691
Glu	Ala	Val	His	Lys	Leu	Leu	Gly	Leu	Pro	Pro	Glu	Ile	Val	Pro	Val	
		185					190						195			
gtg	ggc	ttg	gaa	atg	ggg	cat	gcg	gat	ccg	cct	gaa	cct	gcc	gga	att	739
Val	Gly	Leu	Glu	Met	Gly	His	Ala	Asp	Pro	Pro	Glu	Pro	Ala	Gly	Ile	
		200					205					210				
aaa	cct	ccc	ctg	cca	caa	gaa	gcc	att	gtt	cac	tgg	gat	acc	tac	acc	787
Lys	Pro	Pro	Leu	Pro	Gln	Glu	Ala	Ile	Val	His	Trp	Asp	Thr	Tyr	Thr	
		215				220					225					
gag	aaa	aac	ctc	gaa	ctt	atc	gat	tcc	tac	gac	cgc	gcc	ctc	gac	act	835
Glu	Lys	Asn	Leu	Glu	Leu	Ile	Asp	Ser	Tyr	Asp	Arg	Ala	Leu	Asp	Thr	
	230				235					240					245	
tac	tat	tct	cgc	tac	ggc	cag	cac	cag	ctc	tgg	tcg	aag	cag	acg	gcg	883
Tyr	Tyr	Ser	Arg	Tyr	Gly	Gln	His	Gln	Leu	Trp	Ser	Lys	Gln	Thr	Ala	
			250					255						260		

cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt 931
 His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu
 265 270 275

agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977
 Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg
 280 285

attatggacg cct 990

<210> 792

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 792

Met Gln Gly Asn Ser Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys
 1 5 10 15

Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro
 20 25 30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
 35 40 45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
 50 55 60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
 65 70 75 80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
 85 90 95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
 100 105 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
 115 120 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
 130 135 140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
 145 150 155 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
 165 170 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
 180 185 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
 195 200 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
 210 215 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp

225	230							235							240	
Arg	Ala	Leu	Asp	Thr	Tyr	Tyr	Ser	Arg	Tyr	Gly	Gln	His	Gln	Leu	Trp	
				245					250					255		
Ser	Lys	Gln	Thr	Ala	His	Arg	Ala	Ala	Ser	Lys	Ser	Phe	Ser	Lys	Thr	
			260					265					270			
Asn	Arg	Gln	Phe	Leu	Arg	Gly	Val	Phe	Glu	Arg	Ala	Gly	Phe	Gly	Leu	
		275					280					285				
Arg																

```
<210> 793
<211> 1425
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1402)
<223> RXA00382
```

```

<400> 793
aaaacactat tgaccacccc aatcgctggt gagagtttgt aaagttcgac tgtcaacgag 60

ctggattggc ttcacagatt gaattaatac aatgacgcac atg aca tcg tcc aat 115
Met Thr Ser Ser Asn
1 5

acg gct cga tcc gca gag tgg ttt gaa aag gct cag aag ctc acc cct 163
Thr Ala Arg Ser Ala Glu Trp Phe Glu Lys Ala Gln Lys Leu Thr Pro
10 15 20

ggt ggt gtg aat tct cct gtt cgc gct ttc ggt tca gtt ggc gga caa 211
Gly Gly Val Asn Ser Pro Val Arg Ala Phe Gly Ser Val Gly Gly Gln
25 30 35

gcc cgt ttc atc gaa aaa gct cac ggt tca acg ctg atc gat gtg gac 259
Ala Arg Phe Ile Glu Lys Ala His Gly Ser Thr Leu Ile Asp Val Asp
40 45 50

```

gga	aat	gaa	tac	gtt	gac	ctg	gtc	tgt	tct	tgg	ggc	ccc	atg	ctg	atg	307
Gly	Asn	Glu	Tyr	Val	Asp	Leu	Val	Cys	Ser	Trp	Gly	Pro	Met	Leu	Met	
	55					60					65					
ggt	cac	gct	cac	cca	gca	gtg	gtc	gag	gct	gtg	cag	aag	gcc	gtc	gtg	355
Gly	His	Ala	His	Pro	Ala	Val	Val	Glu	Ala	Val	Gln	Lys	Ala	Val	Val	
	70				75					80					85	
gat	ggt	ctt	tct	ttc	ggc	gct	ccc	acc	atc	ggg	gag	gtt	gag	ttg	gcc	403
Asp	Gly	Leu	Ser	Phe	Gly	Ala	Pro	Thr	Ile	Gly	Glu	Val	Glu	Leu	Ala	
				90					95					100		
caa	gat	atc	gtc	aag	cgc	act	tct	gtg	gag	gaa	gtc	cgc	ctg	gtc	aac	451
Gln	Asp	Ile	Val	Lys	Arg	Thr	Ser	Val	Glu	Glu	Val	Arg	Leu	Val	Asn	
			105					110					115			
tcc	ggc	act	gag	gcc	acc	atg	tcg	gcg	gtt	cgt	ctg	gcg	cgc	ggg	tac	499

Ser Gly Thr Glu Ala Thr Met Ser Ala Val Arg Leu Ala Arg Gly Tyr
 120 125 130

act cag cgt tcc aag att ttg aag ttt gag ggc tgc tac cac ggc cac 547
 Thr Gln Arg Ser Lys Ile Leu Lys Phe Glu Gly Cys Tyr His Gly His
 135 140 145

gtc gat gcg ctg ctc gca tct gct ggt tct ggt gtc gca act ttc gct 595
 Val Asp Ala Leu Leu Ala Ser Ala Gly Ser Gly Val Ala Thr Phe Ala
 150 155 160 165

ctg cct gat tcc cca ggc atc acc ggc gct cag act tct gac act att 643
 Leu Pro Asp Ser Pro Gly Ile Thr Gly Ala Gln Thr Ser Asp Thr Ile
 170 175 180

gtt gtt cct tac aac gac att gaa gcc gtg cgc aac gct ttt gcg gag 691
 Val Val Pro Tyr Asn Asp Ile Glu Ala Val Arg Asn Ala Phe Ala Glu
 185 190 195

tac cca ggc gag atc gcc tgc atc atc gca gag gca gcc ggt ggc aac 739
 Tyr Pro Gly Glu Ile Ala Cys Ile Ile Ala Glu Ala Ala Gly Gly Asn
 200 205 210

atg ggc acc gtc gct cca aag gac aac ttt aac gac aag ctt ctc gcg 787
 Met Gly Thr Val Ala Pro Lys Asp Asn Phe Asn Asp Lys Leu Leu Ala
 215 220 225

atc gct cac gct gac ggc gcg ctg ctg atc ctc gat gaa gtc atg acc 835
 Ile Ala His Ala Asp Gly Ala Leu Leu Ile Leu Asp Glu Val Met Thr
 230 235 240 245

ggc ttc cgc acc tct tac cgt ggc tgg ttc ggc gta gac aag gtt gcc 883
 Gly Phe Arg Thr Ser Tyr Arg Gly Trp Phe Gly Val Asp Lys Val Ala
 250 255 260

gct gac ctg gtc acc ttc ggc aag gtc gtc tcc ggc ggc cta cct gcc 931
 Ala Asp Leu Val Thr Phe Gly Lys Val Val Ser Gly Gly Leu Pro Ala
 265 270 275

gca gcg ttt ggc ggc aag gct gaa atc atg aac atg ctg gcc cca cag 979
 Ala Ala Phe Gly Gly Lys Ala Glu Ile Met Asn Met Leu Ala Pro Gln
 280 285 290

ggc ccc gtc tac caa gca ggc aca ctg tcc ggc aac ccg gtt gcg gtc
 1027
 Gly Pro Val Tyr Gln Ala Gly Thr Leu Ser Gly Asn Pro Val Ala Val
 295 300 305

gca gct ggt cgg gca tcg ctt aag ctt gcc gac gaa tcc ctc tac aca
 1075
 Ala Ala Gly Arg Ala Ser Leu Lys Leu Ala Asp Glu Ser Leu Tyr Thr
 310 315 320 325

acc atc aac gcc aac gca gat cgt ctc cac ggt ttg atc tct gat gcc
 1123
 Thr Ile Asn Ala Asn Ala Asp Arg Leu His Gly Leu Ile Ser Asp Ala
 330 335 340

tta acc cac gaa ggc gta gcc cac cac att cag cgt gcc tca aac atg
 1171
 Leu Thr His Glu Gly Val Ala His His Ile Gln Arg Ala Ser Asn Met

345 350 355
 ctg tct atc cgt ttt gca gaa ggt gag ggc cac aac ttc tct gat atg
 1219
 Leu Ser Ile Arg Phe Ala Glu Gly Glu Gly His Asn Phe Ser Asp Met
 360 365 370
 aag gca gcc gac atc ttc cgc ttc gca ccg ttc ttc cac act ttg ctg
 1267
 Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe Phe His Thr Leu Leu
 375 380 385
 gac aac ggc gtc tac gca cca cca agc gtt ttc gaa acc tgg ttt gtg
 1315
 Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe Glu Thr Trp Phe Val
 390 395 400 405
 tct tcc gct ctc acg gac gat gat ttc tcc aag atc gag cag gca ctc
 1363
 Ser Ser Ala Leu Thr Asp Asp Asp Phe Ser Lys Ile Glu Gln Ala Leu
 410 415 420
 aag ccc gcc gca cgt gca gca gca gaa gcg aag gca tca tgacgcaaac
 1412
 Lys Pro Ala Ala Arg Ala Ala Ala Glu Ala Lys Ala Ser
 425 430
 cattgtccat cta
 1425

<210> 794
 <211> 434
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 794
 Met Thr Ser Ser Asn Thr Ala Arg Ser Ala Glu Trp Phe Glu Lys Ala
 1 5 10 15
 Gln Lys Leu Thr Pro Gly Gly Val Asn Ser Pro Val Arg Ala Phe Gly
 20 25 30

Ser Val Gly Gly Gln Ala Arg Phe Ile Glu Lys Ala His Gly Ser Thr
 35 40 45
 Leu Ile Asp Val Asp Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp
 50 55 60
 Gly Pro Met Leu Met Gly His Ala His Pro Ala Val Val Glu Ala Val
 65 70 75 80
 Gln Lys Ala Val Val Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly
 85 90 95
 Glu Val Glu Leu Ala Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu
 100 105 110
 Val Arg Leu Val Asn Ser Gly Thr Glu Ala Thr Met Ser Ala Val Arg
 115 120 125

Leu Ala Arg Gly Tyr Thr Gln Arg Ser Lys Ile Leu Lys Phe Glu Gly
 130 135 140
 Cys Tyr His Gly His Val Asp Ala Leu Leu Ala Ser Ala Gly Ser Gly
 145 150 155 160
 Val Ala Thr Phe Ala Leu Pro Asp Ser Pro Gly Ile Thr Gly Ala Gln
 165 170 175
 Thr Ser Asp Thr Ile Val Val Pro Tyr Asn Asp Ile Glu Ala Val Arg
 180 185 190
 Asn Ala Phe Ala Glu Tyr Pro Gly Glu Ile Ala Cys Ile Ile Ala Glu
 195 200 205
 Ala Ala Gly Gly Asn Met Gly Thr Val Ala Pro Lys Asp Asn Phe Asn
 210 215 220
 Asp Lys Leu Leu Ala Ile Ala His Ala Asp Gly Ala Leu Leu Ile Leu
 225 230 235 240
 Asp Glu Val Met Thr Gly Phe Arg Thr Ser Tyr Arg Gly Trp Phe Gly
 245 250 255
 Val Asp Lys Val Ala Ala Asp Leu Val Thr Phe Gly Lys Val Val Ser
 260 265 270
 Gly Gly Leu Pro Ala Ala Ala Phe Gly Gly Lys Ala Glu Ile Met Asn
 275 280 285
 Met Leu Ala Pro Gln Gly Pro Val Tyr Gln Ala Gly Thr Leu Ser Gly
 290 295 300
 Asn Pro Val Ala Val Ala Ala Gly Arg Ala Ser Leu Lys Leu Ala Asp
 305 310 315 320
 Glu Ser Leu Tyr Thr Thr Ile Asn Ala Asn Ala Asp Arg Leu His Gly
 325 330 335
 Leu Ile Ser Asp Ala Leu Thr His Glu Gly Val Ala His His Ile Gln
 340 345 350
 Arg Ala Ser Asn Met Leu Ser Ile Arg Phe Ala Glu Gly Glu Gly His
 355 360 365
 Asn Phe Ser Asp Met Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe
 370 375 380
 Phe His Thr Leu Leu Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe
 385 390 395 400
 Glu Thr Trp Phe Val Ser Ser Ala Leu Thr Asp Asp Asp Phe Ser Lys
 405 410 415
 Ile Glu Gln Ala Leu Lys Pro Ala Ala Arg Ala Ala Ala Glu Ala Lys
 420 425 430
 Ala Ser

```
<210> 795
<211> 1233
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1210)
<223> RXA00156
```

<400> 795																
accgagagcg tggtagcgct catttagttt cctcctatga atcttgatgt ggttcatgcg 60																
tttttatgca atatcaacca aaagttggta cgatcctcat atg aat gaa cgc aca 115																
Met Asn Glu Arg Thr 5																
tcg gat gca ttt gac gcc ctc ctt gtg ctc tcc ttc ggt ggt ccc gaa 163																
Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser Phe Gly Gly Pro Glu 20																
ggg cac gag gag gtt cgt ccg ttt ttg gag aat gtc act cac gga agg 211																
Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn Val Thr His Gly Arg 35																
ggg att ccg ccg gaa cgt cta gat gaa gtg gcg gtt cat tac cac cac 259																
Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala Val His Tyr His His 50																
ttc ggt ggt atc agc ccc atc aat gcg ctg aac agg gaa att atc gcc 307																
Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn Arg Glu Ile Ile Ala 65																
aat gtg gaa aaa gaa ttg gcg tct cgc gat cac aag ctg cct gtt tat 355																
Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His Lys Leu Pro Val Tyr 85																
ttt ggt aac cgc aac tgg aag ccg ttt gat aat gag gcc gct gaa caa 403																
Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn Glu Ala Ala Glu Gln 100																
atg gct gat gac ggc gtg aaa aac gcg ctg gtg ttg gca act tcc gct 451																
Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val Leu Ala Thr Ser Ala 105 110 115																
tgg ggt ggc tac tcc ggt tgt cgg cag tac cag gaa gat att cag ggc 499																
Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln Glu Asp Ile Gln Gly 120 125 130																
atg atc aag cac ctg gag tct cag ggg cag tcg atc acg ttc acc aag 547																
Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser Ile Thr Phe Thr Lys 135 140 145																
ctg cgt cag ttc tac gat cac cct cgt ttt gtc tcc acc atg gct caa 595																
Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val Ser Thr Met Ala Gln 150 155 160 165																
ttg gtt cag gat tcc tac gcg aag ctt ccc gat gag ctg cga gat gag 643																
Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp Glu Leu Arg Asp Glu 170 175 180																

gcg cgt ctg gtc ttc acc gcg cac tcc att cca ctg act gcg gac aat 691
 Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro Leu Thr Ala Asp Asn
 185 190 195

gct gcg gga acc cct gag gat ggc tcc ttg tat tcc aca cag gtc aag 739
 Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr Ser Thr Gln Val Lys
 200 205 210

gaa gcg tca gca ctg att gct gag gct gtt ggt gtg tca gat ttt gat 787
 Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly Val Ser Asp Phe Asp
 215 220 225

gtg gtg tgg cag tcc cgc tgc ggt agc ccg cac act ccg tgg ctg gag 835
 Val Val Trp Gln Ser Arg Ser Gly Ser Pro His Thr Pro Trp Leu Glu
 230 235 240 245

cct gac atc gtg gat cac gca gtg gag ctc aac gag aag ggt caa aaa 883
 Pro Asp Ile Val Asp His Ala Val Glu Leu Asn Glu Lys Gly Gln Lys
 250 255 260

gcg ctc gtt gtc tgc cct gta ggc ttt att tct gat cat atg gaa gtc 931
 Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser Asp His Met Glu Val
 265 270 275

att tgg gat ctt gat tcc gag ctg atg gaa gaa gcc gag aag cgc aac 979
 Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu Ala Glu Lys Arg Asn
 280 285 290

atg gtg gtc gag cgt gtc gct acc gtt ggc ccc acc gat gaa ttc gca
 1027
 Met Val Val Glu Arg Val Ala Thr Val Gly Pro Thr Asp Glu Phe Ala
 295 300 305

gcc ctt gtg gtt gat ctc atc gag gag gca gag ctc aag cgc gtt atc
 1075
 Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu Leu Lys Arg Val Ile
 310 315 320 325

gag cgc ctt gga aag ctg cca gca cgc gga agt tcc gtc aac ggc gca
 1123
 Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser Ser Val Asn Gly Ala
 330 335 340

ccg tgt ggc gac ggc tgc tgt ggt acc gcc aag cat aaa acc gcg cgg
 1171
 Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys His Lys Thr Ala Arg
 345 350 355

gtg aac ccc aac gct cgc tca gcg gcg cca gct gcc aac taggagtgat
 1220
 Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala Ala Asn
 360 365 370

agtccctcgc aaa
 1233

<210> 796
 <211> 370
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 796

Met Asn Glu Arg Thr Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser
1 5 10 15

Phe Gly Gly Pro Glu Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn
20 25 30

Val Thr His Gly Arg Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala
35 40 45

Val His Tyr His His Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn
50 55 60

Arg Glu Ile Ile Ala Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His
65 70 75 80

Lys Leu Pro Val Tyr Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn
85 90 95

Glu Ala Ala Glu Gln Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val
100 105 110

Leu Ala Thr Ser Ala Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln
115 120 125

Glu Asp Ile Gln Gly Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser
130 135 140

Ile Thr Phe Thr Lys Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val
145 150 155 160

Ser Thr Met Ala Gln Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp
165 170 175

Glu Leu Arg Asp Glu Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro
180 185 190

Leu Thr Ala Asp Asn Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr
195 200 205

Ser Thr Gln Val Lys Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly
210 215 220

Val Ser Asp Phe Asp Val Val Trp Gln Ser Arg Ser Gly Ser Pro His
225 230 235 240

Thr Pro Trp Leu Glu Pro Asp Ile Val Asp His Ala Val Glu Leu Asn
245 250 255

Glu Lys Gly Gln Lys Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser
260 265 270

Asp His Met Glu Val Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu
275 280 285

Ala Glu Lys Arg Asn Met Val Val Glu Arg Val Ala Thr Val Gly Pro
290 295 300

Thr Asp Glu Phe Ala Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu
305 310 315 320

Leu Lys Arg Val Ile Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser
 325 330 335

Ser Val Asn Gly Ala Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys
 340 345 350

His Lys Thr Ala Arg Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala
 355 360 365

Ala Asn
 370

<210> 797
 <211> 810
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(787)
 <223> RXA00624

<400> 797
 tccatgacgt tttgaatgga aaatctccat ttgtggagtt agaagaagac cactagtttt 60

caacaggacg acaacggccg gacatgacgac aatacaatgc atg tcc ggc cgt ctt 115
 Met Ser Gly Arg Leu
 1 5

ctt gtt tca gtt tct agt att ttc gac cag acc cga tcg gcg gct gac 163
 Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr Arg Ser Ala Ala Asp
 10 15 20

agg ctc att tca gac ctg cga gcc gac ggc atc gag gtc tca tta ctt 211
 Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile Glu Val Ser Leu Leu
 25 30 35

gtc gca ccc cgc atc gat ggg gac tgg cgt ctc gcc aaa gac aaa ggg 259
 Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu Ala Lys Asp Lys Gly
 40 45 50

acc ctc gcg tgg atg gaa caa caa cgc gaa cgc ggc cac gaa ctc atc 307
 Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg Gly His Glu Leu Ile
 55 60 65

ctc aac ggt ttc gac caa gca gtt cag gga cgt cgc tca gaa ttc gcc 355
 Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg Arg Ser Glu Phe Ala
 70 75 80 85

aac ctt gaa cgg cac gaa gca cgt ctt cgc ctt acc ggt gcc att agg 403
 Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu Thr Gly Ala Ile Arg
 90 95 100

caa atg cag aaa att ggc ttc gaa ttc caa atc ttt gcc cca cct cgt 451
 Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile Phe Ala Pro Pro Arg
 105 110 115

tgg aga atg tca gaa ggc acc ttc gcg gta ctc cca gaa ttt gat ttc 499
 Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu Pro Glu Phe Asp Phe

120	125	130	
aac gtc gcc gcc tcg acc agg gga tta cat aac ctc gac acc ggc gaa			547
Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn Leu Asp Thr Gly Glu			
135	140	145	
ttc ttg gcg tgt aga aac ctc tcc gtg ggt gaa ggt ttt ggt gct gca			595
Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu Gly Phe Gly Ala Ala			
150	155	160	165
aaa tgg tgg cgc aag aat gtc atc aag gct gtc act cgt gga gcg gaa			643
Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val Thr Arg Gly Ala Glu			
170	175	180	
aaa gga aat aca gtg cgc ttg tcc gca tcg gcg cga aat ctc acc aac			691
Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala Arg Asn Leu Thr Asn			
185	190	195	
cct aaa gtc gca gct gac ttc cgg gaa gct gca tta gct gcc ttg gat			739
Pro Lys Val Ala Ala Asp Phe Arg Gly Ala Ala Leu Ala Leu Asp			
200	205	210	
ttg ggt gct cag gtg caa acc tat tct cag gcg gcc gca caa ctg gcc			787
Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala Ala Ala Gln Leu Ala			
215	220	225	
tagttgggga ggttcggggc acc			810

<210> 798

<211> 229

<212> PRT

<213> Corynebacterium glutamicum

<400> 798

Met Ser Gly Arg Leu Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr
1 5 10 15

Arg Ser Ala Ala Asp Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile
20 25 30

Glu Val Ser Leu Leu Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu
35 40 45

Ala Lys Asp Lys Gly Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg
50 55 60

Gly His Glu Leu Ile Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg
65 70 75 80

Arg Ser Glu Phe Ala Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu
85 90 95

Thr Gly Ala Ile Arg Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile
100 105 110

Phe Ala Pro Pro Arg Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu
115 120 125

Pro Glu Phe Asp Phe Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn
130 135 140

Leu Asp Thr Gly Glu Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu
145 150 155 160

Gly Phe Gly Ala Ala Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val
165 170 175

Thr Arg Gly Ala Glu Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala
180 185 190

Arg Asn Leu Thr Asn Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala
195 200 205

Leu Ala Ala Leu Asp Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala
210 215 220

Ala Ala Gln Leu Ala
225

<210> 799

<211> 956

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(933)

<223> RXA00306

<400> 799

gat tcc ggc att ccc acg cag ttg gtg gag ggc agc tgg ttt gaa ccg 48
Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
1 5 10 15

gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg 96
Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
20 25 30

gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat 144
Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
35 40 45

cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc 192
Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
50 55 60

aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg 240
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
65 70 75 80

gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt 288
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
85 90 95

tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat 336
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
100 105 110

gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag 384
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu

115	120	125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag			432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys			
130	135	140	
gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa			480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu			
145	150	155	160
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag			528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln			
165	170		175
tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc			576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg			
180	185		190
acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc			624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg			
195	200		205
ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat			672
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp			
210	215		220
gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc			720
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg			
225	230	235	240
acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc			768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser			
245	250		255
atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg			816
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu			
260	265		270
gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac			864
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn			
275	280		285
ggc gcc att gcg gcg ttg gta gat ctc atc cgc cac gga ttg gta ttg			912
Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu			
290	295	300	
ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag			956
Pro Ala Asp Leu Leu Asp Ser			
305	310		

<210> 800

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 800

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro

1

5

10

15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val

20	25	30
Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp		
35	40	45
Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu		
50	55	60
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala		
65	70	75
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly		
85	90	95
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr		
100	105	110
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu		
115	120	125
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys		
130	135	140
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu		
145	150	155
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln		
165	170	175
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg		
180	185	190
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg		
195	200	205
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp		
210	215	220
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg		
225	230	235
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser		
245	250	255
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu		
260	265	270
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn		
275	280	285
Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu		
290	295	300
Pro Ala Asp Leu Leu Asp Ser		
305	310	

<210> 801

<211> 1263

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1240)

<223> RXA00884

<400> 801

catcttccgt ttcataccct gcactctacc ctgttcttag gaattcgcta tgtttaacat 60

caattaatca tgtatagggg gcaggcacta ggcttggggc atg tca gtt ttt ggt 115
 Met Ser Val Phe Gly
 1 5

gtg tat att cat gtg ccg ttt tgt tca act cgg tgc ggt tat tgc gat 163
 Val Tyr Ile His Val Pro Phe Cys Ser Thr Arg Cys Gly Tyr Cys Asp
 10 15 20

ttc aac acc tat act gct ggg gaa tta ggt agt act gca ggc ccg gac 211
 Phe Asn Thr Tyr Thr Ala Gly Glu Leu Gly Ser Thr Ala Gly Pro Asp
 25 30 35

acc tat ctt gac tcg ttg gaa gtt gag ttg gag atg gct gtg gct tcg 259
 Thr Tyr Leu Asp Ser Leu Glu Val Glu Leu Glu Met Ala Val Ala Ser
 40 45 50

ctg gat aat cct cgg cag gcg gaa act atc ttt att ggc ggg ggt acc 307
 Leu Asp Asn Pro Arg Gln Ala Glu Thr Ile Phe Ile Gly Gly Gly Thr
 55 60 65

ccg tcg ttg att ggt gcg gac ggt ttg gcc agg gtt ttg ggg gct gtg 355
 Pro Ser Leu Ile Gly Ala Asp Gly Leu Ala Arg Val Leu Gly Ala Val
 70 75 80 85

cgc aat act ttt ggc att gcg gat ggt gcg gaa gtc acc acg gag tcc 403
 Arg Asn Thr Phe Gly Ile Ala Asp Gly Ala Glu Val Thr Thr Glu Ser
 90 95 100

aat ccg gag tct acc tcg cct gag ttt ttt gat ggc ctg cgt gag gcg 451
 Asn Pro Glu Ser Thr Ser Pro Glu Phe Phe Asp Gly Leu Arg Glu Ala
 105 110 115

ggc tac aac agg att tcg tta ggg atg cag tcg gcg tcg tca agc gtt 499
 Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser Ala Ser Ser Val
 120 125 130

ttg aag gtg ctg gac cgc acg cac acc cca ggg cgc ccg gtg gcg gcg 547
 Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly Arg Pro Val Ala Ala
 135 140 145

gcc aag gag gca cgt gag gcg ggg ttt gag cat gtc aat ttg gac atg 595
 Ala Lys Glu Ala Arg Glu Ala Gly Phe Glu His Val Asn Leu Asp Met
 150 155 160 165

att tat ggc acg ccg aca gag acc gat gat gat gtc cgc aag acg ctg 643
 Ile Tyr Gly Thr Pro Thr Glu Thr Asp Asp Asp Val Arg Lys Thr Leu
 170 175 180

aat gcg gtg ctc gaa gcg aac gtg gat cac gtg tct gcc tat tcc ttg 691
 Asn Ala Val Leu Glu Ala Asn Val Asp His Val Ser Ala Tyr Ser Leu
 185 190 195

atc gtg aaa gat ggc acg gcg atg gcg cgc aag gtg cac aag ggc gag 739
 Ile Val Lys Asp Gly Thr Ala Met Ala Arg Lys Val His Lys Gly Glu
 200 205 210

ctg cca gcg ccg gac gag gat gtc tac gct gat cgt ttt gag ctt atc 787
 Leu Pro Ala Pro Asp Glu Asp Val Tyr Ala Asp Arg Phe Glu Leu Ile
 215 220 225

gac gct cgc ctg cgc tca gct ggt ttc gat tgg tac gag gtg tcc aac 835
 Asp Ala Arg Leu Arg Ser Ala Gly Phe Asp Trp Tyr Glu Val Ser Asn
 230 235 240 245

tgg gcg aaa ccc ggc gga gaa tgc aag cac aac atg ggc tat tgg gtc 883
 Trp Ala Lys Pro Gly Gly Glu Cys Lys His Asn Met Gly Tyr Trp Val
 250 255 260

gac ggc gac tgg tgg ggc gcg ggc ccg ggc gcg cac tcg cac atc ggc 931
 Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala His Ser His Ile Gly
 265 270 275

gac cgc cgc ttc tac aac atc aag cac cca gcg cgt tac tcc gcg cag 979
 Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala Arg Tyr Ser Ala Gln
 280 285 290

att gcg gcc ggc gag ctg ccc att aag gaa aca gag cgg ctg acg gcg
 1027
 Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr Glu Arg Leu Thr Ala
 295 300 305

gaa gat cac cac acc gag cgc gtc atg ctt ggt ttg cgc ctg aaa caa
 1075
 Glu Asp His His Thr Glu Arg Val Met Leu Gly Leu Arg Leu Lys Gln
 310 315 320 325

ggc gtg ccg ctg aac ctt ttc gca ccc gca gcg cgc ccg gtc atc gac
 1123
 Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala Arg Pro Val Ile Asp
 330 335 340

cgt cat atc gca ggg ggc ctg ctg cac gtc aat gcg ctg ggc aac ctg
 1171
 Arg His Ile Ala Gly Gly Leu Leu His Val Asn Ala Leu Gly Asn Leu
 345 350 355

gcg gtg acc gat gcg gga cgt ttg ctt gcc gac ggc atc atc gcc gac
 1219
 Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp Gly Ile Ile Ala Asp
 360 365 370

att ttg ctt agt gaa gaa gac taaatattta gtaggggttac aga
 1263
 Ile Leu Leu Ser Glu Glu Asp
 375 380

<210> 802

<211> 380

<212> PRT

<213> Corynebacterium glutamicum

<400> 802

Met Ser Val Phe Gly Val Tyr Ile His Val Pro Phe Cys Ser Thr Arg
 1 5 10 15
 Cys Gly Tyr Cys Asp Phe Asn Thr Tyr Thr Ala Gly Glu Leu Gly Ser
 20 25 30
 Thr Ala Gly Pro Asp Thr Tyr Leu Asp Ser Leu Glu Val Glu Leu Glu
 35 40 45
 Met Ala Val Ala Ser Leu Asp Asn Pro Arg Gln Ala Glu Thr Ile Phe
 50 55 60
 Ile Gly Gly Gly Thr Pro Ser Leu Ile Gly Ala Asp Gly Leu Ala Arg
 65 70 75 80
 Val Leu Gly Ala Val Arg Asn Thr Phe Gly Ile Ala Asp Gly Ala Glu
 85 90 95
 Val Thr Thr Glu Ser Asn Pro Glu Ser Thr Ser Pro Glu Phe Phe Asp
 100 105 110
 Gly Leu Arg Glu Ala Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser
 115 120 125
 Ala Ser Ser Ser Val Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly
 130 135 140
 Arg Pro Val Ala Ala Ala Lys Glu Ala Arg Glu Ala Gly Phe Glu His
 145 150 155 160
 Val Asn Leu Asp Met Ile Tyr Gly Thr Pro Thr Glu Thr Asp Asp Asp
 165 170 175
 Val Arg Lys Thr Leu Asn Ala Val Leu Glu Ala Asn Val Asp His Val
 180 185 190
 Ser Ala Tyr Ser Leu Ile Val Lys Asp Gly Thr Ala Met Ala Arg Lys
 195 200 205
 Val His Lys Gly Glu Leu Pro Ala Pro Asp Glu Asp Val Tyr Ala Asp
 210 215 220
 Arg Phe Glu Leu Ile Asp Ala Arg Leu Arg Ser Ala Gly Phe Asn Trp
 225 230 235 240
 Tyr Glu Val Ser Asn Trp Ala Lys Pro Gly Gly Glu Cys Lys His Asn
 245 250 255
 Met Gly Tyr Trp Val Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala
 260 265 270
 His Ser His Ile Gly Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala
 275 280 285
 Arg Tyr Ser Ala Gln Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr
 290 295 300
 Glu Arg Leu Thr Ala Glu Asp His His Thr Glu Arg Val Met Leu Gly
 305 310 315 320
 Leu Arg Leu Lys Gln Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala

```

          325          330          335
Arg Pro Val Ile Asp Arg His Ile Ala Gly Gly Leu Leu His Val Asn
          340          345          350
Ala Leu Gly Asn Leu Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp
          355          360          365
Gly Ile Ile Ala Asp Ile Leu Leu Ser Glu Glu Asp
          370          375          380

<210> 803
<211> 522
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(499)
<223> RXN02503

<400> 803
gcagcaccgg caaccacgtc cgtcaacgcg tcagaactgc cggatgcggg ttcgctcgca 60
ttcgtgaacg caccttctgc cacacaaacg agggagtaac atg acc tta aaa att 115
                               Met Thr Leu Lys Ile
                               1           5

ggt acc cga gga tcc aaa ctt gcc acc acc caa gct ggc acc atc cgc 163
Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln Ala Gly Thr Ile Arg
          10          15          20

gac cag ctg aaa cac tac gga cgc gac gct gaa ctg cac atc gtg acc 211
Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu Leu His Ile Val Thr
          25          30          35

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259
Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly
          40          45          50

gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307
Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp
          55          60          65

gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355
Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg
          70          75          80          85

ttc cac ctg gtc gtg cca act cgt gcg gac tcg cgc gag gcc ctt atc 403
Phe His Leu Val Val Pro Thr Arg Ala Asp Ser Arg Glu Ala Leu Ile
          90          95          100

gcc cgc gac ggc ctg act ctg gct gag ctt cca gaa agg cgc aaa ggt 451
Ala Arg Asp Gly Leu Thr Leu Ala Glu Leu Pro Glu Arg Arg Lys Gly
          105          110          115

ggg aac ttc cgc tcc tcg acg cat ctc cca gct caa ggc aat ccg ccc 499
Gly Asn Phe Arg Ser Ser Thr His Leu Pro Ala Gln Gly Asn Pro Pro
          120          125          130

```

tgacctggag attctccac tgc

522

<210> 804

<211> 133

<212> PRT

<213> Corynebacterium glutamicum

<400> 804

Met	Thr	Leu	Lys	Ile	Gly	Thr	Arg	Gly	Ser	Lys	Leu	Ala	Thr	Thr	Gln
1				5					10					15	

Ala	Gly	Thr	Ile	Arg	Asp	Gln	Leu	Lys	His	Tyr	Gly	Arg	Asp	Ala	Glu
			20						25				30		

Leu	His	Ile	Val	Thr	Thr	Pro	Gly	Asp	Val	Asn	Met	Ser	Pro	Val	Glu
		35					40					45			

Arg	Ile	Gly	Val	Gly	Val	Phe	Thr	Gln	Ala	Leu	Arg	Asp	Val	Leu	His
	50					55					60				

Ser	Gly	Glu	Cys	Asp	Val	Ala	Val	His	Ser	Met	Lys	Asp	Leu	Pro	Thr
65					70					75					80

Ala	Thr	Asp	Pro	Arg	Phe	His	Leu	Val	Val	Pro	Thr	Arg	Ala	Asp	Ser
				85					90					95	

Arg	Glu	Ala	Leu	Ile	Ala	Arg	Asp	Gly	Leu	Thr	Leu	Ala	Glu	Leu	Pro
		100						105					110		

Glu	Arg	Arg	Lys	Gly	Gly	Asn	Phe	Arg	Ser	Ser	Thr	His	Leu	Pro	Ala
	115						120					125			

Gln	Gly	Asn	Pro	Pro
	130			

<210> 805

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA02503

<400> 805

gcagcaccgg caaccacgtc cgtcaacgcg tcagaactgc cggatgcggg tatcgctcgca 60

ttcgtgaacg	caccttctgc	cacacaaacg	aggagtaac	atg	acc	tta	aaa	att	115
				Met	Thr	Leu	Lys	Ile	
				1				5	

ggt	acc	cga	gga	tcc	aaa	ctt	gcc	acc	acc	caa	gct	ggc	acc	atc	cgc	163
Gly	Thr	Arg	Gly	Ser	Lys	Leu	Ala	Thr	Thr	Gln	Ala	Gly	Thr	Ile	Arg	
				10					15					20		

gac	cag	ctg	aaa	cac	tac	gga	cgc	gac	gct	gaa	ctg	cac	atc	gtg	acc	211
Asp	Gln	Leu	Lys	His	Tyr	Gly	Arg	Asp	Ala	Glu	Leu	His	Ile	Val	Thr	
			25					30					35			

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259
 Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly
 40 45 50

gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307
 Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp
 55 60 65

gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355
 Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg
 70 75 80 85

ttc cac ctg gtc gtg cca act cgt gcg gac tck cgc cga ggs cct tat 403
 Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa Arg Arg Xaa Pro Tyr
 90 95 100

cgc ccn cga cgg sct gan ttt kgg ttr agc tty caa aar gsg saa agg 451
 Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa Gln Xaa Xaa Xaa Arg
 105 110 115

tgg gaa ctt tcc gct cct cga cgc atc tcc cag ctc aag gca atc cgc 499
 Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg
 120 125 130

cct gac ctg gag att ctc cca ctt gcg cgg aaa cat tgacaccggc 545
 Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys His
 135 140 145

atgggcaagg tca 558

<210> 806

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 806

Met Thr Leu Lys Ile Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln
 1 5 10 15

Ala Gly Thr Ile Arg Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu
 20 25 30

Leu His Ile Val Thr Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu
 35 40 45

Arg Ile Gly Val Gly Val Phe Thr Gln Ala Leu Arg Asp Val Leu His
 50 55 60

Ser Gly Glu Cys Asp Val Ala Val His Ser Met Lys Asp Leu Pro Thr
 65 70 75 80

Ala Thr Asp Pro Arg Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa
 85 90 95

Arg Arg Xaa Pro Tyr Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa
 100 105 110

Gln Xaa Xaa Xaa Arg Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln
 115 120 125

Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys
 130 135 140

His
 145

<210> 807
 <211> 1245
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1222)
 <223> RXA00377

<400> 807
 aatggcgctc gggcagggcg cgcaagtact aaccagcaat tcccaagccc aaaaaccct 60

cccatatagt tctttttact gatgcattgt cctcaattag gtg tgg ctt ctt ttc 115
 Val Trp Leu Leu Phe
 1 5

cta aat tgg gat aaa tgg ggc aag att gag cgc atg tct gct ctt act 163
 Leu Asn Trp Asp Lys Trp Gly Lys Ile Glu Arg Met Ser Ala Leu Thr
 10 15 20

att cca gct gcg cgt cgc acg cta aat aac gcg ccc att att gat gcc 211
 Ile Pro Ala Ala Arg Arg Thr Leu Asn Asn Ala Pro Ile Ile Asp Ala
 25 30 35

gct aat ggc aag acc ccg act cgc act ccg gtg tgg ttt atg cgc cag 259
 Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val Trp Phe Met Arg Gln
 40 45 50

gcg ggt agg tcg ttg cct gag tac aag aag gtc cgt gag gga atc agc 307
 Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val Arg Glu Gly Ile Ser
 55 60 65

atg ttg gat tcc tgt ttc atg ccg gag ttg ttg gcg gag att act ttg 355
 Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu Ala Glu Ile Thr Leu
 70 75 80 85

cag ccg gtt cgt cgt cat gat gtg gat gct gcg att ttg ttc tct gac 403
 Gln Pro Val Arg Arg His Asp Val Asp Ala Ala Ile Leu Phe Ser Asp
 90 95 100

att gtg gtg ccg ttg cgt gct gcg ggt gtt ggt gtg gaa atc gtg gcg 451
 Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly Val Glu Ile Val Ala
 105 110 115

ggt cgt gga cct gtg ttg gat gcg ccg gtg cgg agc cgt ggg gat gtg 499
 Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg Ser Arg Gly Asp Val
 120 125 130

ttg aat ctt cct att ttg gag ggc aac gtt ccg gag gtg gag cag ggt 547
 Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro Glu Val Glu Gln Gly
 135 140 145

att ggc atc att ttg gat gag ttg tct gat tct cag gcg ttg att ggt 595
 Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser Gln Ala Leu Ile Gly
 150 155 160 165

ttt gct ggt gcg ccg ttt acg ttg gcg agt tac ttg gtt gag ggt ggt 643
 Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr Leu Val Glu Gly Gly
 170 175 180

cct tcc aag aat cat gag aag acc aaa gca atg atg cat ggt gat cct 691
 Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met Met His Gly Asp Pro
 185 190 195

gag acg tgg cat gcg ttg atg gct cgt ttg gtg ccg acg att gtg aat 739
 Glu Thr Trp His Ala Leu Met Ala Arg Leu Val Pro Thr Ile Val Asn
 200 205 210

tct ttg aag tcg cag atc gat gcg ggt atc gat gcg gtg cag ttg ttt 787
 Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp Ala Val Gln Leu Phe
 215 220 225

gat tcg tgg gct ggg ttc ctc act gag cgt gat tac acc gag ttc gtg 835
 Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp Tyr Thr Glu Phe Val
 230 235 240 245

ttg ccg tat tcc act gag att ttg gag gaa gtg ggc aag tac cag ctg 883
 Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val Gly Lys Tyr Gln Leu
 250 255 260

cct cgt att cac ttt ggt gtg ggt act ggt gag ttg ctt ggt gcg atg 931
 Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu Leu Leu Gly Ala Met
 265 270 275

agc aag gct ggc tca gag gtc atg ggt gtg gat tgg ccg gtg ccg ttg 979
 Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp Trp Arg Val Pro Leu
 280 285 290

gat aag gct gcg gag cgt att gct gcg gta tca ggt cct aag gtg ttg
 1027
 Asp Lys Ala Ala Glu Arg Ile Ala Ala Val Ser Gly Pro Lys Val Leu
 295 300 305

cag ggt aac ctc gat cct gcg ttg ttg ttt gcg ggt cgc gca cct ttg
 1075
 Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala Gly Arg Ala Pro Leu
 310 315 320 325

act aag gaa att gag cgc atc aag gca gag gct cag act gct gtt gat
 1123
 Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala Gln Thr Ala Val Asp
 330 335 340

gca ggt cat gca acg ggc cat atc ttt aac ctt ggt cat ggt gtg ctt
 1171
 Ala Gly His Ala Thr Gly His Ile Phe Asn Leu Gly His Gly Val Leu
 345 350 355

cct aat acg gtg gcg gaa gat att act gaa gcc gtc tcc atc att cat
 1219
 Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala Val Ser Ile Ile His
 360 365 370

tct taaactaaga ggagtttcat gcg
1245
Ser

<210> 808
<211> 374
<212> PRT
<213> Corynebacterium glutamicum

<400> 808
Val Trp Leu Leu Phe Leu Asn Trp Asp Lys Trp Gly Lys Ile Glu Arg
1 5 10 15
Met Ser Ala Leu Thr Ile Pro Ala Ala Arg Arg Thr Leu Asn Asn Ala
20 25 30
Pro Ile Ile Asp Ala Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val
35 40 45
Trp Phe Met Arg Gln Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val
50 55 60
Arg Glu Gly Ile Ser Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu
65 70 75 80
Ala Glu Ile Thr Leu Gln Pro Val Arg Arg His Asp Val Asp Ala Ala
85 90 95
Ile Leu Phe Ser Asp Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly
100 105 110
Val Glu Ile Val Ala Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg
115 120 125
Ser Arg Gly Asp Val Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro
130 135 140
Glu Val Glu Gln Gly Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser
145 150 155 160
Gln Ala Leu Ile Gly Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr
165 170 175
Leu Val Glu Gly Gly Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met
180 185 190
Met His Gly Asp Pro Glu Thr Trp His Ala Leu Met Ala Arg Leu Val
195 200 205
Pro Thr Ile Val Asn Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp
210 215 220
Ala Val Gln Leu Phe Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp
225 230 235 240
Tyr Thr Glu Phe Val Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val
245 250 255
Gly Lys Tyr Gln Leu Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu

260 265 270
 Leu Leu Gly Ala Met Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp
 275 280 285
 Trp Arg Val Pro Leu Asp Lys Ala Ala Glu Arg Ile Ala Ala Val Ser
 290 295 300
 Gly Pro Lys Val Leu Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala
 305 310 315 320
 Gly Arg Ala Pro Leu Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala
 325 330 335
 Gln Thr Ala Val Asp Ala Gly His Ala Thr Gly His Ile Phe Asn Leu
 340 345 350
 Gly His Gly Val Leu Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala
 355 360 365
 Val Ser Ile Ile His Ser
 370

 <210> 809
 <211> 681
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(658)
 <223> RXN02504

 <400> 809
 cctcgattcc acctggtcgt gccaaactcgt gcggactcgc gcgaggccct tatcgcccg 60

 gacggcctga ctctggctga gcttcagaa aggcgcaaag gtg gga act tcc gct 115
 Val Gly Thr Ser Ala
 1 5

 cct cga cgc atc tcc cag ctc aag gca atc cgc cct gac ctg gag att 163
 Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile
 10 15 20

 ctc cca ctg cgc gga aac att gac acc ggc atg ggc aag gtc acc tcc 211
 Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met Gly Lys Val Thr Ser
 25 30 35

 ggt gaa ctc gat gct gtg atg ctc gcc tac gca ggc ctc acc cgc gtc 259
 Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala Gly Leu Thr Arg Val
 40 45 50

 ggc atg cag gac cgc gca acg gaa gtt ttc gac gcc gac atc atc atg 307
 Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp Ala Asp Ile Ile Met
 55 60 65

 ccc gcc ccc gca cag ggc gca ctt gcg atc gaa tgc cgc gcc gac gac 355
 Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp
 70 75 80 85

act gaa acc gtc cgc gcg ctc aac atg ctg atg cac gcc gac acg ttt 403
 Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe
 90 95 100

gtt tcc gcg gtt gca gaa cgc acc gtg ctc aac cgc ctc gaa gct ggc 451
 Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly
 105 110 115

tgt acc gcg cct gtc gca gcg cac gcc acc ttg gac ggc tac tcc ggc 499
 Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly
 120 125 130

gac acc atg act ctc acc gcc ggc gtc tac gca ctt gac ggc tct gac 547
 Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp
 135 140 145

cag ctg gta ttc tcc gcc gaa ggt gac ggc gcc cgc cca gaa gag ctc 595
 Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu
 150 155 160 165

ggc gag ctc gtt gca caa cag ctt atc gac gcc gga gcc gcc aat ttg 643
 Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu
 170 175 180

ctc ggc gac cgc agc taattagggc ccgaaatttc cat 681
 Leu Gly Asp Arg Ser
 185

<210> 810

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 810

Val Gly Thr Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg
 1 5 10 15

Pro Asp Leu Glu Ile Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met
 20 25 30

Gly Lys Val Thr Ser Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala
 35 40 45

Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp
 50 55 60

Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu
 65 70 75 80

Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met
 85 90 95

His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn
 100 105 110

Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu
 115 120 125

Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala
 130 135 140

Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala
145 150 155 160

Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala
165 170 175

Gly Ala Ala Asn Leu Leu Gly Asp Arg Ser
180 185

<210> 811

<211> 561

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(538)

<223> FRXA02504

<400> 811

gcatacctcca gctcaaggca atccgccctg acctggagat tctccactt gcgcggaaac 60

attgacaccg gcataggcaa ggtcacctcc ggtgaactcg atg ctt gtg atg ctc 115
Met Leu Val Met Leu
1 5

gcc tac gca ggc ctc acc cgc gtc ggc atg cag gac cgc gca acg gaa 163
Ala Tyr Ala Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu
10 15 20

gtt ttc gac gcc gac atc atc atg ccc gcc ccc gca cag ggc gca ctt 211
Val Phe Asp Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu
25 30 35

gcg atc gaa tgc cgc gcc gac gac act gaa acc gtc cgc gcg ctc aac 259
Ala Ile Glu Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn
40 45 50

atg ctg atg cac gcc gac acg ttt gtt tcc gcg gtt gca gaa cgc acc 307
Met Leu Met His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr
55 60 65

gtg ctc aac cgc ctc gaa gct ggc tgt acc gcg cct gtc gca gcg cac 355
Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His
70 75 80 85

gcc acc ttg gac ggc tac tcc ggc gac acc atg act ctc acc gcc ggc 403
Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly
90 95 100

gtc tac gca ctt gac ggc tct gac cag ctg gta ttc tcc gcc gaa ggt 451
Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly
105 110 115

gac ggc gcc cgc cca gaa gag ctc ggc gag ctc gtt gca caa cag ctt 499
Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu
120 125 130

atc gac gcc gga gcc gcc aat ttg ctc ggc gac cgc agc taattagggc 548

Ile Asp Ala Gly Ala Ala Asn Leu Leu Gly Asp Arg Ser
 135 140 145

ccgaaatttc cat

561

<210> 812
 <211> 146
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 812
 Met Leu Val Met Leu Ala Tyr Ala Gly Leu Thr Arg Val Gly Met Gln
 1 5 10 15

Asp Arg Ala Thr Glu Val Phe Asp Ala Asp Ile Ile Met Pro Ala Pro
 20 25 30

Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp Thr Glu Thr
 35 40 45

Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe Val Ser Ala
 50 55 60

Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala
 65 70 75 80

Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met
 85 90 95

Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val
 100 105 110

Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu
 115 120 125

Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu Leu Gly Asp
 130 135 140

Arg Ser
 145

<210> 813
 <211> 1449
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1426)
 <223> RXN01162

<400> 813
 catcgaatac gtgccctgct gaatagatga catcgagag atctataaga gtcagtgggtt 60

gtcgggggttt cacagtcact tattctatgc aggattcacc atg tat atc gtg ggg 115
 Met Tyr Ile Val Gly
 1 5

att tgt cta caa tta gtg gtt atg agc caa ccg atg tca gca ccc gac 163

Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro Met Ser Ala Pro Asp	
10 15 20	
tcc gct cca gga aca gag cgc ggt cat gaa cgc acc cat ttt gcg gta	211
Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg Thr His Phe Ala Val	
25 30 35	
gtc ggt gac tcc cag gat cca gca cag gca aca gct cct aga gcg cca	259
Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr Ala Pro Arg Ala Pro	
40 45 50	
gca gaa tca att act ttg att ggt att ggt acc gat ggg ttt gag ggg	307
Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr Asp Gly Phe Glu Gly	
55 60 65	
ctc gga ctc aag gca cag caa gca tta caa cgt gcc tct gtg gtg att	355
Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg Ala Ser Val Val Ile	
70 75 80 85	
gga tca tgg cgc cag ctc aat ctc gta cct gat gcc att aag gca gag	403
Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp Ala Ile Lys Ala Glu	
90 95 100	
cgt cgc cca tgg ccg ggt aat acc aag cat cct gat tta gat gcc ttg	451
Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro Asp Leu Asp Ala Leu	
105 110 115	
ttt aaa gag ttc ctc ggt cgg cat gtt gct gtt ctg gcc tct ggc gat	499
Phe Lys Glu Phe Leu Gly Arg His Val Ala Val Leu Ala Ser Gly Asp	
120 125 130	
cca ctg ttt tac ggc gtg ggc acc gca atg gtc cat gtg ctg ggg atg	547
Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val His Val Leu Gly Met	
135 140 145	
gat aga ctc acg gtt att ccg gga cca tca tcc gcg tcg ctt gct tgc	595
Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser Ala Ser Leu Ala Cys	
150 155 160 165	
gcc cgc ttg ggt tgg aca gtc aac cgc aca cgg gtg gtg tac cta gga	643
Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg Val Val Tyr Leu Gly	
170 175 180	
caa gaa ccc att gag aca ctc atc ccg att att gaa tca ggc gct caa	691
Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile Glu Ser Gly Ala Gln	
185 190 195	
ttc ctc gtc ttg ggt aaa gat gaa ttc agt aca gct caa gtt gcc acg	739
Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr Ala Gln Val Ala Thr	
200 205 210	
ttg ttg aat gaa ctc gga ctg ggg gag act cca ctg act gtg ctc agc	787
Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro Leu Thr Val Leu Ser	
215 220 225	
gat ttg ggc agt act gat gag gag atc acc caa ggc aca gct tca cat	835
Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln Gly Thr Ala Ser His	
230 235 240 245	
cca cca gct gca gtg tct gtt ctc aac gtg att gct gtg gga gct cgc	883
Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile Ala Val Gly Ala Arg	

250	255	260	
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac			931
Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp			
265	270	275	
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg			979
Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met			
280	285	290	
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta			
1027			
Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu			
295	300	305	
cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt			
1075			
Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val			
310	315	320	325
gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt			
1123			
Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser			
330	335	340	
gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta			
1171			
Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val			
345	350	355	
caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc			
1219			
Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly			
360	365	370	
cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct			
1267			
Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro			
375	380	385	
gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag			
1315			
Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys			
390	395	400	405
ctt cac aca ctc caa gaa caa cac ggc gga atc atc aaa cac atc cgc			
1363			
Leu His Thr Leu Gln Glu Gln His Gly Gly Ile Ile Lys His Ile Arg			
410	415	420	
atc gac gac aca gac gtg cac caa tgg cga gtt aca aag ccg gtg act			
1411			
Ile Asp Asp Thr Asp Val His Gln Trp Arg Val Thr Lys Pro Val Thr			
425	430	435	
cca gaa gcg gtg aat tagcatcaaaa aaccaacccc atg			
1449			
Pro Glu Ala Val Asn			
440			

<210> 814

<211> 442

<212> PRT

<213> Corynebacterium glutamicum

<400> 814

```

Met Tyr Ile Val Gly Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro
  1           5           10           15

Met Ser Ala Pro Asp Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg
          20           25           30

Thr His Phe Ala Val Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr
          35           40           45

Ala Pro Arg Ala Pro Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr
          50           55           60

Asp Gly Phe Glu Gly Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg
          65           70           75           80

Ala Ser Val Val Ile Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp
          85           90           95

Ala Ile Lys Ala Glu Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro
          100          105          110

Asp Leu Asp Ala Leu Phe Lys Glu Phe Leu Gly Arg His Val Ala Val
          115          120          125

Leu Ala Ser Gly Asp Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val
          130          135          140

His Val Leu Gly Met Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser
          145          150          155          160

Ala Ser Leu Ala Cys Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg
          165          170          175

Val Val Tyr Leu Gly Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile
          180          185          190

Glu Ser Gly Ala Gln Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr
          195          200          205

Ala Gln Val Ala Thr Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro
          210          215          220

Leu Thr Val Leu Ser Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln
          225          230          235          240

Gly Thr Ala Ser His Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile
          245          250          255

Ala Val Gly Ala Arg Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp
          260          265          270

Val Ser Asn Glu Asp Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro
          275          280          285

Thr Gln Gly Gln Met Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu

```

290 295 300

Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser
305 310 315 320

Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly
325 330 335

Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys
340 345 350

Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile
355 360 365

Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp
370 375 380

Met Met Leu Arg Pro Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu
385 390 395 400

Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly Ile
405 410 415

Ile Lys His Ile Arg Ile Asp Asp Thr Asp Val His Gln Trp Arg Val
420 425 430

Thr Lys Pro Val Thr Pro Glu Ala Val Asn
435 440

<210> 815

<211> 1345

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1345)

<223> FRXA01162

<400> 815

catcgaatac gtgccctgct gaatagatga catcgcagag atctataaga gtcagtgggtt 60

gtcgggggttt cacagtcact tattctatgc aggattcacc atg tat atc gtg ggg 115
Met Tyr Ile Val Gly
1 5

att tgt cta caa tta gtg gtt atg agc caa ccg atg tca gca ccc gac 163
Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro Met Ser Ala Pro Asp
10 15 20

tcc gct cca gga aca gag cgc ggt cat gaa cgc acc cat ttt gcg gta 211
Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg Thr His Phe Ala Val
25 30 35

gtc ggt gac tcc cag gat cca gca cag gca aca gct cct aga gcg cca 259
Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr Ala Pro Arg Ala Pro
40 45 50

gca gaa tca att act ttg att ggt att ggt acc gat ggg ttt gag ggg 307
Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr Asp Gly Phe Glu Gly

55	60	65	
ctc gga ctc aag gca cag caa gca tta caa cgt gcc tct gtg gtg att			355
Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg Ala Ser Val Val Ile			
70	75	80	85
gga tca tgg cgc cag ctc aat ctc gta cct gat gcc att aag gca gag			403
Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp Ala Ile Lys Ala Glu			
90	95		100
cgt cgc cca tgg ccg ggt aat acc aag cat cct gat tta gat gcc ttg			451
Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro Asp Leu Asp Ala Leu			
105	110		115
ttt aaa gag ttc ctc ggt cgg cat gtt gct gtt ctg gcc tct ggc gat			499
Phe Lys Glu Phe Leu Gly Arg His Val Ala Val Leu Ala Ser Gly Asp			
120	125		130
cca ctg ttt tac ggc gtg ggc acc gca atg gtc cat gtg ctg ggg atg			547
Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val His Val Leu Gly Met			
135	140		145
gat aga ctc acg gtt att ccg gga cca tca tcc gcg tcg ctt gct tgc			595
Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser Ala Ser Leu Ala Cys			
150	155		160
gcc cgc ttg ggt tgg aca gtc aac cgc aca cgg gtg gtg tac cta gga			643
Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg Val Val Tyr Leu Gly			
170	175		180
caa gaa ccc att gag aca ctc atc ccg att att gaa tca ggc gct caa			691
Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile Glu Ser Gly Ala Gln			
185	190		195
ttc ctc gtc ttg ggt aaa gat gaa ttc agt aca gct caa gtt gcc acg			739
Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr Ala Gln Val Ala Thr			
200	205		210
ttg ttg aat gaa ctc gga ctg ggg gag act cca ctg act gtg ctc agc			787
Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro Leu Thr Val Leu Ser			
215	220		225
gat ttg ggc agt act gat gag gag atc acc caa ggc aca gct tca cat			835
Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln Gly Thr Ala Ser His			
230	235		240
cca cca gct gca gtg tct gtt ctc aac gtg att gct gtg gga gct cgc			883
Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile Ala Val Gly Ala Arg			
250	255		260
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac			931
Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp			
265	270		275
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg			979
Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met			
280	285		290
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta			
1027			
Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu			

295 300 305
 cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt
 1075
 Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val
 310 315 320 325
 gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt
 1123
 Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser
 330 335 340
 gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta
 1171
 Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val
 345 350 355
 caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc
 1219
 Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly
 360 365 370
 cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct
 1267
 Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro
 375 380 385
 gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag
 1315
 Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys
 390 395 400 405
 ctt cac aca ctc caa gaa caa cac ggc gga
 1345
 Leu His Thr Leu Gln Glu Gln His Gly Gly
 410 415
 <210> 816
 <211> 415
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 816
 Met Tyr Ile Val Gly Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro
 1 5 10 15
 Met Ser Ala Pro Asp Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg
 20 25 30
 Thr His Phe Ala Val Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr
 35 40 45
 Ala Pro Arg Ala Pro Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr
 50 55 60
 Asp Gly Phe Glu Gly Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg
 65 70 75 80
 Ala Ser Val Val Ile Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp
 85 90 95

Ala Ile Lys Ala Glu Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro
 100 105 110
 Asp Leu Asp Ala Leu Phe Lys Glu Phe Leu Gly Arg His Val Ala Val
 115 120 125
 Leu Ala Ser Gly Asp Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val
 130 135 140
 His Val Leu Gly Met Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser
 145 150 155 160
 Ala Ser Leu Ala Cys Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg
 165 170 175
 Val Val Tyr Leu Gly Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile
 180 185 190
 Glu Ser Gly Ala Gln Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr
 195 200 205
 Ala Gln Val Ala Thr Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro
 210 215 220
 Leu Thr Val Leu Ser Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln
 225 230 235 240
 Gly Thr Ala Ser His Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile
 245 250 255
 Ala Val Gly Ala Arg Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp
 260 265 270
 Val Ser Asn Glu Asp Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro
 275 280 285
 Thr Gln Gly Gln Met Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu
 290 295 300
 Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser
 305 310 315 320
 Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly
 325 330 335
 Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys
 340 345 350
 Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile
 355 360 365
 Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp
 370 375 380
 Met Met Leu Arg Pro Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu
 385 390 395 400
 Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly
 405 410 415

```
<220>  
<221> CDS  
<222> (101)..(850)  
<223> RXA01692
```

1130

atc atg ggt gtg aaa aat gcg ggt gcg att gcc cag gcg ctc atg gac 691
 Ile Met Gly Val Lys Asn Ala Gly Ala Ile Ala Gln Ala Leu Met Asp
 185 190 195

ggc ggg ctt gat gca gat act cca gca gct gtt att cag gaa ggc act 739
 Gly Gly Leu Asp Ala Asp Thr Pro Ala Ala Val Ile Gln Glu Gly Thr
 200 205 210

act gat gca caa cgc tca gtt cgg tgc acc ttg ggc aca ttg ggt gca 787
 Thr Asp Ala Gln Arg Ser Val Arg Cys Thr Leu Gly Thr Leu Gly Ala
 215 220 225

gtc atg gtg gag gaa gag att aag cct cca gct gtg tat gtc att gga 835
 Val Met Val Glu Glu Ile Lys Pro Pro Ala Val Tyr Val Ile Gly
 230 235 240 245

caa gtt gct ggc ctc taagcagatc gcctaagaat ggg 873
 Gln Val Ala Gly Leu
 250

<210> 818

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 818

Met Thr Ile Ser Gln Glu Asn Gln Pro Ile Ile Gln Pro Val Ser Leu
 1 5 10 15

Ile Gly Gly Gly Pro Gly Ala Trp Asp Leu Ile Thr Val Arg Gly Met
 20 25 30

Asn Arg Leu Gln Glu Ala Asp Val Ile Leu Ala Asp His Leu Gly Pro
 35 40 45

Thr Asp Glu Leu Glu Lys Leu Cys Asp Ile Ser Ser Lys Thr Val Val
 50 55 60

Asp Val Ser Lys Leu Pro Tyr Gly Arg Gln Val Thr Gln Glu Arg Thr
 65 70 75 80

Asn Glu Met Leu Val Glu Tyr Ala Gln Gln Gly Leu Lys Val Val Arg
 85 90 95

Leu Lys Gly Gly Asp Pro Tyr Val Phe Gly Arg Gly Phe Glu Glu Leu
 100 105 110

Glu Phe Leu Gly Glu His Gly Ile Glu Cys Glu Val Ile Pro Gly Val
 115 120 125

Thr Ser Ala Val Ser Val Pro Ala Ala Ala Gly Ile Pro Ile Thr Asn
 130 135 140

Arg Gly Val Val His Ser Phe Thr Val Val Ser Gly His Leu Pro Pro
 145 150 155 160

Gly His Pro Lys Ser Leu Val Asp Trp Ala Ala Leu Ala Lys Ser Gly
 165 170 175

Gly Thr Leu Ser Ile Ile Met Gly Val Lys Asn Ala Gly Ala Ile Ala
 180 185 190

Gln Ala Leu Met Asp Gly Gly Leu Asp Ala Asp Thr Pro Ala Ala Val
 195 200 205

Ile Gln Glu Gly Thr Thr Asp Ala Gln Arg Ser Val Arg Cys Thr Leu
 210 215 220

Gly Thr Leu Gly Ala Val Met Val Glu Glu Glu Ile Lys Pro Pro Ala
 225 230 235 240

Val Tyr Val Ile Gly Gln Val Ala Gly Leu
 245 250

<210> 819

<211> 1917

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1894)

<223> RXN00371

<400> 819

gtcgtggaca atcccggatc gaaaatttga ttcggctttt ttcattggctg ttgatggagt 60

acgttgggtcg ttttcgagac aagtactaga aaagatattg atg act atc gcc cat 115
 Met Thr Ile Ala His
 1 5

aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163
 Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser
 10 15 20

gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211
 Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val
 25 30 35

tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259
 Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro
 40 45 50

ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307
 Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu
 55 60 65

aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355
 Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr
 70 75 80 85

gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403
 Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile
 90 95 100

cct gtg ccg gaa gat aag ctt cag gct gcg gaa gat gag tac gag cgc 451
 Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu Asp Glu Tyr Glu Arg
 105 110 115

atc tgc att gaa gcg aag gag aac ggt gca cgc cgt aag cct cct cgt 499
 ile Cys ile Glu Ala Lys Glu Asn Gly Ala Arg Arg Lys Pro Pro Arg
 120 125 130

cca gca cca cca acc gct gca gag atc acg gaa gtt tct gag gcg act 547
 Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu Val Ser Glu Ala Thr
 135 140 145

cca gct cag att gtt gag ctt gtg cag gat gct ctt tct tat ggt gga 595
 Pro Ala Gln ile Val Glu Leu Val Gln Asp Ala Leu Ser Tyr Gly Gly
 150 155 160 165

gat gtt att cgt ctt gtc acc ggc aac cca ttg agc agc gat gcc aca 643
 Asp Val ile Arg Leu Val Thr Gly Asn Pro Leu Ser Ser Asp Ala Thr
 170 175 180

ctg gct gag atc tct gca gtt tcc gag gct ggc ctg gag ttc cag gtg 691
 Leu Ala Glu ile Ser Ala Val Ser Glu Ala Gly Leu Glu Phe Gln Val
 185 190 195

gtt cca ggt atg tct ttg cct gca acg gtt cct gca ttt gcg gga att 739
 Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro Ala Phe Ala Gly ile
 200 205 210

gcg ttg ggt tct acc tac acc gaa act gat gtc aac ggt caa aac ttg 787
 Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val Asn Gly Gln Asn Leu
 215 220 225

gac tgg gat cag ttg gct agc gca cct cag cct ttg gtg ctg cag gcc 835
 Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro Leu Val Leu Gln Ala
 230 235 240 245

cgc gtg gat gac ctt tcc cgt att gca cag gaa cta aag gcc cgc aat 883
 Arg Val Asp Asp Leu Ser Arg ile Ala Gln Glu Leu Lys Ala Arg Asn
 250 255 260

atg tct ttg gaa act cct gtt tct gtc acc gct aac ggc acc acc cgt 931
 Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala Asn Gly Thr Thr Arg
 265 270 275

ttg cag cgc acc tat gac acc act tta ggt ctg ttg cac aag ctt gat 979
 Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu Leu His Lys Leu Asp
 280 285 290

gct gaa cta agc gga cct ttg gtt gtt acc ttg ggc aag ggt gtg gat
 1027
 Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu Gly Lys Gly Val Asp
 295 300 305

gat cgc tcc aag tac tct tgg tgg gaa aac cgc gct ctg tac ggt tgg
 1075
 Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg Ala Leu Tyr Gly Trp
 310 315 320 325

cgt gtg ctg gtg cct cgc gct cgg gag caa gcg gca tcc atg tcc gca
 1123
 Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala Ala Ser Met Ser Ala
 330 335 340

cgt ctg agc agc cac ggc gct atc ccg cag gaa gtc cct acc att tct
 1171

Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu Val Pro Thr Ile Ser
345 350 355

gtc gaa cca ccg cgc aac cca gcg caa atg gaa cgc gcc atc aag ggc
1219

Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala Ile Lys Gly
360 365 370

atc gtc gaa gga cgc tac cag tgg gtt gtc ctc acc agc gtc aac gca
1267

Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser Val Asn Ala
375 380 385

gtg aag gca gtc tgg gag aaa atc acc gaa ttc ggc ctc gat tca cgt
1315

Val Lys Ala Val Trp Glu Lys Ile Thr Glu Phe Gly Leu Asp Ser Arg
390 395 400 405

tcc ttc gcg ggc gtc cgc atc gcc gca gtc ggt gaa aaa acc gcc gct
1363

Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys Thr Ala Ala
410 415 420

gag atc cgc gcg ctc ggc atc acg ccg gag ctt ctg cct gca cgt acc
1411

Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro Ala Arg Thr
425 430 435

agg caa aat gcg caa ggg ctt gtc gac gtg ttc ccc gaa tat ttc gaa
1459

Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu Tyr Phe Glu
440 445 450

gaa ctc gat cca gtc ggc cgt gtc ctc ttg ccg cgc gca gat atc gca
1507

Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala Asp Ile Ala
455 460 465

acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg gaa gtc gaa
1555

Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp Glu Val Glu
470 475 480 485

gac gtg gtg gct tac cgc acc gtc cgc gca gca cca cca agc gct gat
1603

Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro Ser Ala Asp
490 495 500

atc cga gat atg atc aag acc ggc gga ttt gat gca gtt gcc ttc acc
1651

Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val Ala Phe Thr
505 510 515

tct tcg tcg acc gtg aag aac ctc gtt ggt atc gcg ggt aaa cca cac
1699

Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly Lys Pro His
520 525 530

cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca gcg acc gct
1747

Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala Ala Thr Ala

<400> 820																
Met	Thr	Ile	Ala	His	Lys	Pro	Glu	Met	Ala	Glu	Thr	Thr	Gly	Ile	Glu	
1				5					10					15		
Thr	Asn	Gln	Val	Ser	Glu	Thr	Ile	Gly	Val	Glu	Ser	Leu	Thr	His	Gly	
			20					25					30			
Asn	Leu	Arg	Pro	Val	Ser	Ser	Phe	Glu	Gly	Gln	His	Glu	Gly	Gln	Thr	
		35					40					45				
Glu	Glu	Leu	Leu	Pro	Gly	Lys	Val	Ile	Phe	Val	Gly	Ala	Gly	Pro	Gly	
	50					55					60					
Asn	Pro	Asp	Leu	Leu	Thr	Val	Arg	Ala	Arg	Glu	Val	Leu	Gly	Asn	Ala	
65					70					75					80	
Val	Arg	Ala	Ile	Thr	Asp	Glu	Gln	Val	Leu	Ser	Gly	Val	Arg	Ala	Phe	
			85						90					95		
Val	Ala	Thr	Glu	Ile	Pro	Val	Pro	Glu	Asp	Lys	Leu	Gln	Ala	Ala	Glu	
			100					105					110			
Asp	Glu	Tyr	Glu	Arg	Ile	Cys	Ile	Glu	Ala	Lys	Glu	Asn	Gly	Ala	Arg	
	115					120						125				
Arg	Lys	Pro	Pro	Arg	Pro	Ala	Pro	Pro	Thr	Ala	Ala	Glu	Ile	Thr	Glu	
	130					135					140					
Val	Ser	Glu	Ala	Thr	Pro	Ala	Gln	Ile	Val	Glu	Leu	Val	Gln	Asp	Ala	
145					150					155					160	
Leu	Ser	Tyr	Gly	Gly	Asp	Val	Ile	Arg	Leu	Val	Thr	Gly	Asn	Pro	Leu	
			165					170							175	

Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly
 180 185 190
 Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro
 195 200 205
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val
 210 215 220
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro
 225 230 235 240
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu
 245 250 255
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala
 260 265 270
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu
 275 280 285
 Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu
 290 295 300
 Gly Lys Gly Val Asp Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg
 305 310 315 320
 Ala Leu Tyr Gly Trp Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala
 325 330 335
 Ala Ser Met Ser Ala Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu
 340 345 350
 Val Pro Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu
 355 360 365
 Arg Ala Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu
 370 375 380
 Thr Ser Val Asn Ala Val Lys Ala Val Trp Glu Lys Ile Thr Glu Phe
 385 390 395 400
 Gly Leu Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly
 405 410 415
 Glu Lys Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu
 420 425 430
 Leu Pro Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe
 435 440 445
 Pro Glu Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro
 450 455 460
 Arg Ala Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu
 465 470 475 480
 Gly Trp Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala
 485 490 495

Pro Pro Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp
500 505 510

Ala Val Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile
515 520 525

Ala Gly Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met
530 535 540

Thr Ala Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro
545 550 555 560

Glu Ile Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val
565 570 575

Ala Asp Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg
580 585 590

Arg Arg Arg Lys Ala Ser
595

<210> 821

<211> 1024

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1024)

<223> FRXA00371

<400> 821

gtcgtggaca atcccgatc gaaaatttga ttcggctttt ttcattggctg ttgatggagt 60

acgttggtcg ttttcgagac aagtactaga aaagatattg atg act atc gcc cat 115
Met Thr Ile Ala His
1 5

aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163
Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser
10 15 20

gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211
Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val
25 30 35

tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259
Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro
40 45 50

ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307
Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu
55 60 65

aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355
Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr
70 75 80 85

gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403
Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile

	90	95	100	
cct gtg ccg gaa gat aag ctt cag gct gcg gaa gat gag tac gag cgc				451
Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu Asp Glu Tyr Glu Arg				
	105	110	115	
atc tgc att gaa gcg aag gag aac ggt gca cgc cgt aag cct cct cgt				499
Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg Arg Lys Pro Pro Arg				
	120	125	130	
cca gca cca cca acc gct gca gag atc acg gaa gtt tct gag gcg act				547
Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu Val Ser Glu Ala Thr				
	135	140	145	
cca gct cag att gtt gag ctt gtg cag gat gct ctt tct tat ggt gga				595
Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala Leu Ser Tyr Gly Gly				
	150	155	160	165
gat gtt att cgt ctt gtc acc ggc aac cca ttg agc agc gat gcc aca				643
Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu Ser Ser Asp Ala Thr				
	170	175		180
ctg gct gag atc tct gca gtt tcc gag gct ggc ctg gag ttc cag gtg				691
Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly Leu Glu Phe Gln Val				
	185	190		195
gtt cca ggt atg tct ttg cct gca acg gtt cct gca ttt gcg gga att				739
Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro Ala Phe Ala Gly Ile				
	200	205	210	
gcg ttg ggt tct acc tac acc gaa act gat gtc aac ggt caa aac ttg				787
Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val Asn Gly Gln Asn Leu				
	215	220	225	
gac tgg gat cag ttg gct agc gca cct cag cct ttg gtg ctg cag gcc				835
Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro Leu Val Leu Gln Ala				
	230	235	240	245
cgc gtg gat gac ctt tcc cgt att gca cag gaa cta aag gcc cgc aat				883
Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu Leu Lys Ala Arg Asn				
	250	255	260	
atg tct ttg gaa act cct gtt tct gtc acc gct aac ggc acc acc cgt				931
Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala Asn Gly Thr Thr Arg				
	265	270	275	
ttg cag cgc acc tat gac acc act tta ggt ctg ttg cac aag ctt gat				979
Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu Leu His Lys Leu Asp				
	280	285	290	
gct gaa cta agc gga cct ttg gtt gtt acc ttg ggc aag ggt gtg				
1024				
Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu Gly Lys Gly Val				
	295	300	305	

<210> 822

<211> 308

<212> PRT

<213> Corynebacterium glutamicum

<400> 822

Met Thr Ile Ala His Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu
 1 5 10 15

Thr Asn Gln Val Ser Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly
 20 25 30

Asn Leu Arg Pro Val Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr
 35 40 45

Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly
 50 55 60

Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala
 65 70 75 80

Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe
 85 90 95

Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu
 100 105 110

Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg
 115 120 125

Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu
 130 135 140

Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala
 145 150 155 160

Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu
 165 170 175

Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly
 180 185 190

Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro
 195 200 205

Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val
 210 215 220

Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro
 225 230 235 240

Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu
 245 250 255

Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala
 260 265 270

Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu
 275 280 285

Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu
 290 295 300

Gly Lys Gly Val
 305

<210> 823
 <211> 755
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(732)
 <223> FRXA00374

<400> 823
 acc att tct gtc gaa cca ccg cgc aac cca gcg caa atg gaa cgc gcc 48
 Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala
 1 5 10 15
 atc aag ggc atc gtc gaa gga cgc tac cag tgg gtt gtc ctc aca agc 96
 Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser
 20 25 30
 gtc aac gca gtg aag gca gtc tgg aag aaa atc acc gaa ttc ggc ctc 144
 Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu
 35 40 45
 gat tca cgt tcc ttc gcg ggc gtc cgc atc gcc gca gtc ggt gaa aaa 192
 Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys
 50 55 60
 acc gcc gct gag atc cgc gcg ctc ggc atc acg ccg gag ctt ctg cct 240
 Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro
 65 70 75 80
 gca cgt acc agg caa aat gcg caa ggg ctt gtc gac gtg ttc ccc gaa 288
 Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu
 85 90 95
 tat ttc gaa gaa ctc gat cca gtc ggc cgt gtc ctc ttg ccg cgc gca 336
 Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala
 100 105 110
 gat atc gca acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg 384
 Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp
 115 120 125

gaa gtc gaa gac gtg gtg gct tac cgc acc gtc cgc gca gca cca cca 432
 Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro
 130 135 140
 agc gct gat atc cga gat atg atc aag acc ggc gga ttt gat gca gtt 480
 Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val
 145 150 155 160
 gcc ttc acc tct tcg tcg acc gtg aag aac ctc gtt ggt atc gcg ggt 528
 Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly
 165 170 175
 aaa cca cac cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca 576
 Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala
 180 185 190
 gcg acc gct gaa gaa ctg gga ctg cgc gtt gat gtc atg cca gag atc 624

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile
 195 200 205

gcc gaa gta cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat 672
 Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp
 210 215 220

ctg cgc gct aag ggc gag ctg ccg ccg ccg agg aag aaa cgc agg cgt 720
 Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg
 225 230 235 240

cga aaa gcg tct taaaagggtt ttcactaggg tgt 755
 Arg Lys Ala Ser

<210> 824
 <211> 244
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 824
 Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala
 1 5 10 15

Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser
 20 25 30

Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu
 35 40 45

Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys
 50 55 60

Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro
 65 70 75 80

Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu
 85 90 95

Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala
 100 105 110

Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp
 115 120 125

Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro
 130 135 140

Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val
 145 150 155 160

Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly
 165 170 175

Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala
 180 185 190

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile
 195 200 205

Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp
 210 215 220

Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg
 225 230 235 240

Arg Lys Ala Ser

<210> 825

<211> 1467

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1444)

<223> RXN00383

<400> 825

ccatatcttt aaccttggtc atggtgtgct tcctaatacgtgtggcggaag atattactga 60

agccgtctcc atcattcatt cttaaactaa gaggagtttc atg cgt ttt gcc atc 115
 Met Arg Phe Ala Ile
 1 5

atc ggt gca ggc ctt gcg ggt ctg act gct gca tat gag atc cat aaa 163
 Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala Tyr Glu Ile His Lys
 10 15 20

gct gat ccc act gcc caa atc gat gtg ttg gaa gca ggc gaa cgc att 211
 Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu Ala Gly Glu Arg Ile
 25 30 35

ggc ggc aag ctt ttt acg gtg ccg ttt gct tcc gga cct acc gat att 259
 Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser Gly Pro Thr Asp Ile
 40 45 50

gga gcg gag gcg ttt tta gct gcg cgt tcc gat gcg gtg gag ttt ttt 307
 Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp Ala Val Glu Phe Phe
 55 60 65

act gag ctt ggg ttg gct gat tct ttg gtc agc ccg tct gct gcg aag 355
 Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser Pro Ser Ala Ala Lys
 70 75 80 85

tct cag tat ttc gcg ggc ggt gcg ctg cat gcg ttc ccc gca ggt gga 403
 Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala Phe Pro Ala Gly Gly
 90 95 100

gtg atg ggt att cca agc aat cca cca gca ggc gcg caa gac acc gct 451
 Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly Ala Gln Asp Thr Ala
 105 110 115

ttt gat tgg act cct ggc caa gac att tct gtt ggc gcc tta gtg cgc 499
 Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val Gly Ala Leu Val Arg
 120 125 130

cgt cag tat ggc gat gag atc gtc gat act gtg gtg tct tcg ctg ctt 547
 Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val Val Ser Ser Leu Leu

135	140	145	
ggt ggc gtt tat tcc tcc acc gct gat gat ctg ggt gtg cgc gct tcc			595
Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu Gly Val Arg Ala Ser			
150	155	160	165
gtg ccg gca ctt gct gca gcc ctt gat cag ctg gct gag gcc ggc gag			643
Val Pro Ala Leu Ala Ala Ala Leu Asp Gln Leu Ala Glu Ala Gly Glu			
	170	175	180
ccg gtg act ctg tca gct gcg gtc aag gcc gtg gaa gct cag cgg gaa			691
Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val Glu Ala Gln Arg Glu			
	185	190	195
gcc gca aaa aca act tca gaa acc cgc ccc gtt ttc cag acc ttc aag			739
Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val Phe Gln Thr Phe Lys			
	200	205	210
ggc gga tac gcg gag ctg tac gaa gcg ttg gca gag caa tgc ggt gca			787
Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala Glu Gln Cys Gly Ala			
	215	220	225
gat att cac ttg gat agt ttc gtt tcc gcc atc acc aaa gat ggt gaa			835
Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile Thr Lys Asp Gly Glu			
	230	235	240
ggt ttt gcc atc aag ggc ggt ggc gaa ggc acc tac gac aag gtg att			883
Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr Tyr Asp Lys Val Ile			
	250	255	260
ttg gcg gtt ccc gct cca acc gcc gct gtg ctg ctc cgc gac ttg gca			931
Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu Leu Arg Asp Leu Ala			
	265	270	275
ccg gcc gca gcg cca cat ttg cgc gca att aag ttg gct tct tca gca			979
Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys Leu Ala Ser Ser Ala			
	280	285	290
gtc gtc ggc atg cgt ttc gat tcc agc gag ggc ctg ccc gac aac tcc			
1027			
Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly Leu Pro Asp Asn Ser			
	295	300	305
ggc gtc ctg gtc gct gtt aat gag ccg ggc atc acg gcg aag gcc ttc			
1075			
Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile Thr Ala Lys Ala Phe			
	310	315	320
acg ttc tcc tca aag aag tgg cct cac ctg gag gct cgc ggg ggc gcg			
1123			
Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu Ala Arg Gly Gly Ala			
	330	335	340
ctc gtg cgc gcg tcg ttc ggc agg cta ggc gat gag gcg tcg gca cgc			
1171			
Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp Glu Ala Ser Ala Arg			
	345	350	355
atg gac gag gat ttg ctt gtc gac gcc gcc ctc gac gat ctc ctc acc			
1219			
Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu Asp Asp Leu Leu Thr			

360 365 370
 ata acc ggg ttc gac ggc cgg gct gcc gga ctg ggt gaa att ttc gtg
 1267
 Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu Gly Glu Ile Phe Val
 375 380 385
 cag cgc tgg ttc ggt ggg ctc cca gcc tat gga gtt gat cac att gct
 1315
 Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly Val Asp His Ile Ala
 390 395 400 405
 acc gtt tcg gct gcg cgt gca gag atc gca gcc gtg cct ggc gtg gaa
 1363
 Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala Val Pro Gly Val Glu
 410 415 420
 gca att ggc gcg tgg gct ggg gga gtg gga gtt ccc gca gtt atc gca
 1411
 Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val Pro Ala Val Ile Ala
 425 430 435
 gat gcc cag gca gca gta cac agg ttg ctg gga taagcaccca aaaacactat
 1464
 Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly
 440 445
 tga
 1467

<210> 826
 <211> 448
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 826
 Met Arg Phe Ala Ile Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala
 1 5 10 15
 Tyr Glu Ile His Lys Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu
 20 25 30

Ala Gly Glu Arg Ile Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser
 35 40 45
 Gly Pro Thr Asp Ile Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp
 50 55 60
 Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser
 65 70 75 80
 Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala
 85 90 95
 Phe Pro Ala Gly Gly Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly
 100 105 110
 Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val
 115 120 125

Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val
 130 135 140
 Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu
 145 150 155 160
 Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp Gln Leu
 165 170 175
 Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val
 180 185 190
 Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val
 195 200 205
 Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala
 210 215 220
 Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile
 225 230 235 240
 Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr
 245 250 255
 Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu
 260 265 270
 Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys
 275 280 285
 Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly
 290 295 300
 Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile
 305 310 315 320
 Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu
 325 330 335
 Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp
 340 345 350
 Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu
 355 360 365
 Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu
 370 375 380
 Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly
 385 390 395 400
 Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala
 405 410 415
 Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val
 420 425 430
 Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly
 435 440 445

<210> 827
 <211> 382
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(382)
 <223> FRXA00376

<400> 827
 ccatactcttt aaccttggtc atggtgtgct tcctaatacg gtggcggaag atattactga 60
 agccgtctcc atcattcatt cttaaactaa gaggagtttc atg cgt ttt gcc atc 115
 Met Arg Phe Ala Ile
 1 5
 atc ggt gca ggc ctt gcg ggt ctg act gct gca tat gag atc cat aaa 163
 Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala Tyr Glu Ile His Lys
 10 15 20
 gct gat ccc act gcc caa atc gat gtg ttg gaa gca ggc gaa cgc att 211
 Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu Ala Gly Glu Arg Ile
 25 30 35
 ggc ggc aag ctt ttt acg gtg ccg ttt gct tcc gga cct acc gat att 259
 Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser Gly Pro Thr Asp Ile
 40 45 50
 gga gcg gag gcg ttt tta gct gcg cgt tcc gat gcg gtg gag ttt ttt 307
 Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp Ala Val Glu Phe Phe
 55 60 65
 act gag ctt ggg ttg gct gat tct ttg gtc agc ccg tct gct gcg aag 355
 Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser Pro Ser Ala Ala Lys
 70 75 80 85
 tct cag tat ttc gcg ggc ggt gcg ctg 382
 Ser Gln Tyr Phe Ala Gly Gly Ala Leu
 90

<210> 828
 <211> 94
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 828
 Met Arg Phe Ala Ile Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala
 1 5 10 15
 Tyr Glu Ile His Lys Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu
 20 25 30
 Ala Gly Glu Arg Ile Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser
 35 40 45
 Gly Pro Thr Asp Ile Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp

50 55 60
 Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser
 65 70 75 80
 Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu
 85 90

 <210> 829
 <211> 1037
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (1)..(1014)
 <223> FRXA00383

 <400> 829
 gca ggc gcg caa gac acc gct ttt gat tgg act cct ggc caa gac att 48
 Ala Gly Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile
 1 5 10 15

 tct gtt ggc gcc tta gtg cgc cgt cag tat ggc gat gag atc gtc gat 96
 Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp
 20 25 30

 act gtg gtg tct tcg ctg ctt ggt ggc gtt tat tcc tcc acc gct gat 144
 Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp
 35 40 45

 gat ctg ggt gtg cgc gct tcc gtg ccg gca ctt gct gca gcc ctt gat 192
 Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp
 50 55 60

 cag ctg gct gag gcc ggc gag ccg gtg act ctg tca gct gcg gtc aag 240
 Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys
 65 70 75 80

 gcc gtg gaa gct cag cgg gaa gcc gca aaa aca act tca gaa acc cgc 288
 Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg
 85 90 95

 ccc gtt ttc cag acc ttc aag ggc gga tac gcg gag ctg tac gaa gcg 336
 Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala
 100 105 110

 ttg gca gag caa tgc ggt gca gat att cac ttg gat agt ttc gtt tcc 384
 Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser
 115 120 125

 gcc atc acc aaa gat ggt gaa ggt ttt gcc atc aag ggc ggt ggc gaa 432
 Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu
 130 135 140

 ggc acc tac gac aag gtg att ttg gcg gtt ccc gct cca acc gcc gct 480
 Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala
 145 150 155 160

 gtg ctg ctc cgc gac ttg gca ccg gcc gca gcg cca cat ttg cgc gca 528

Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala
 165 170 175

att aag ttg gct tct tca gca gtc gtc ggc atg cgt ttc gat tcc agc 576
 Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser
 180 185 190

gag ggc ctg ccc gac aac tcc ggc gtc ctg gtc gct gtt aat gag ccg 624
 Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro
 195 200 205

ggc atc acg gcg aag gcc ttc acg ttc tcc tca aag aag tgg cct cac 672
 Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His
 210 215 220

ctg gag gct cgc ggg ggc gcg ctc gtg cgc gcg tcg ttc ggc agg cta 720
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu
 225 230 235 240

ggc gat gag gcg tcg gca cgc atg gac gag gat ttg ctt gtc gac gcc 768
 Gly Asp Glu Ala Ser Arg Met Asp Glu Asp Leu Leu Val Asp Ala
 245 250 255

gcc ctc gac gat ctc ctc acc ata acc ggg ttc gac ggc cgg gct gcc 816
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala
 260 265 270

gga ctg ggt gaa att ttc gtg cag cgc tgg ttc ggt ggg ctc cca gcc 864
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala
 275 280 285

tat gga gtt gat cac att gct acc gtt tcg gct gcg cgt gca gag atc 912
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile
 290 295 300

gca gcc gtg cct ggc gtg gaa gca att ggc gcg tgg gct ggg gga gtg 960
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val
 305 310 315 320

gga gtt ccc gca gtt atc gca gat gcc cag gca gca gta cac agg ttg
 1008

Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu
 325 330 335

ctg gga taagcaccca aaaacactat tga
 1037
 Leu Gly

<210> 830

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 830

Ala Gly Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile
 1 5 10 15

Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp
 20 25 30

Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp
 35 40 45
 Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Leu Asp
 50 55 60
 Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys
 65 70 75 80
 Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg
 85 90 95
 Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala
 100 105 110
 Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser
 115 120 125
 Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu
 130 135 140
 Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala
 145 150 155 160
 Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala
 165 170 175
 Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser
 180 185 190
 Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro
 195 200 205
 Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His
 210 215 220
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu
 225 230 235 240
 Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala
 245 250 255
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala
 260 265 270
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala
 275 280 285
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile
 290 295 300
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val
 305 310 315 320
 Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu
 325 330 335
 Leu Gly

```
<220>  
<221> CDS  
<222> (101)..(850)  
<223> RXA01253
```

1150

tcc gaa aac acc gac gac caa cgc caa caa ttc gcc gaa ggc gcc gtc 691
 Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe Ala Glu Gly Ala Val
 185 190 195
 caa ggc agc atc atc gcc acc tac atg cac ggc ccc gca ctc gcc cga 739
 Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly Pro Ala Leu Ala Arg
 200 205 210
 aac ccc caa ctc gcc gac ctc atg ctc gca aaa gca atg ggt gtc gcg 787
 Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys Ala Met Gly Val Ala
 215 220 225
 ctg aaa gac ctg gag cct ttg gac atc gac gtc atc gac cgc ctc cgc 835
 Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val Ile Asp Arg Leu Arg
 230 235 240 245
 gcc gaa cgc ctg gcg tagcccttc taaaccgggt cta 873
 Ala Glu Arg Leu Ala
 250

<210> 832

<211> 250

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 832

Met Thr Thr Leu Asn Ile Gly Leu Ile Leu Pro Asp Val Leu Gly Thr
 1 5 10 15
 Tyr Gly Asp Asp Gly Asn Ala Leu Val Leu Arg Gln Arg Ala Arg Met
 20 25 30
 Arg Gly Ile Asn Ala Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val
 35 40 45
 Pro Ser Thr Leu Asp Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala
 50 55 60
 Gln Ile Leu Ala Thr Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr
 65 70 75 80
 Ala Ala Ala Ala Gly Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln
 85 90 95
 Val Leu Gly Asp Ser Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu
 100 105 110
 Gly Leu Ile Asp Ala Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly
 115 120 125
 Glu Val Glu Thr Thr Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr
 130 135 140
 Glu Arg Leu Thr Gly Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly
 145 150 155 160
 Pro Asp Ala Glu Pro Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr
 165 170 175

Asp Val Trp Ala Ala Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe
 180 185 190

Ala Glu Gly Ala Val Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly
 195 200 205

Pro Ala Leu Ala Arg Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys
 210 215 220

Ala Met Gly Val Ala Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val
 225 230 235 240

Ile Asp Arg Leu Arg Ala Glu Arg Leu Ala
 245 250

<210> 833

<211> 1044

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1021)

<223> RXA02134

<400> 833

tgatgaacga catgtcgaca ttttcttcg cggcgctcga tggacccta aacgcctctt 60

ccgaagcgcc cgagcaaac acggagtaac tttctaagcg atg tcc ggc aaa gca 115
 Met Ser Gly Lys Ala
 1 5

ggc ttt acc ccc gaa gat ccc gaa gac tca gac aac cgc cac ggg aac 163
 Gly Phe Thr Pro Glu Asp Pro Glu Asp Ser Asp Asn Arg His Gly Asn
 10 15 20

ccc ctt ttc gaa ggt atc ttt acc gca ctt aat tgg atg acc gtt ctc 211
 Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn Trp Met Thr Val Leu
 25 30 35

ccc gtc ccc ggc gca tca gtt ttt gat cgc acc acg ggc gcc cgg gta 259
 Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr Thr Gly Ala Arg Val
 40 45 50

atg gcc tct ttg ccc ttt gtt ggc ttc gtt ttc gga atg ttc acc gcg 307
 Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe Gly Met Phe Thr Ala
 55 60 65

atc atc atg tgg gct atc ggc ccc att tca ggg gtg atc cac gtc gat 355
 Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly Val Ile His Val Asp
 70 75 80 85

gga ctt tta gtt gcc gtt ctg atc gtc gcg ttc tgg gaa ctt ctt aat 403
 Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe Trp Glu Leu Leu Asn
 90 95 100

cgg ttt atg cac ctc gac ggc ctc gca gat gtc tcc gat gct ttg ggt 451
 Arg Phe Met His Leu Asp Gly Leu Ala Asp Val Ser Asp Ala Leu Gly
 105 110 115

tcc tac gca gcc cca cca cgc gca cga gaa atc ctt gcc gat ccc cgc 499
 Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile Leu Ala Asp Pro Arg
 120 125 130

acc gga ctt ttc ggc ctc gcc acc gcc atg ctt tcc gtt ctc ctg cag 547
 Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu Ser Val Leu Leu Gln
 135 140 145

gtc gct gca gtc gca tcg ctt gtc gat tca acc gtg tgg tgg atg atc 595
 Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr Val Trp Trp Met Ile
 150 155 160 165

tgc ttc atc ccc gtt ctc ggc cgc atc gct gga caa gta acc gca ctg 643
 Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly Gln Val Thr Ala Leu
 170 175 180

aaa aac cac aac gcc ttc tcc ccc acc ggc ttt ggc gca cta gtc atc 691
 Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe Gly Ala Leu Val Ile
 185 190 195

gga acg gtg aaa ttt tgg tgg atc gcg ctg tgg ctc ttg gtt act gct 739
 Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp Leu Leu Val Thr Ala
 200 205 210

gcg ttg gct ttt tgg tgc gca gaa tta att tct cca ctt tca ccg ctg 787
 Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser Pro Leu Ser Pro Leu
 215 220 225

acc agt gtt aac act ccc ttt gtc gct gga cct ttc ccc gct gca atc 835
 Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro Phe Pro Ala Ala Ile
 230 235 240 245

aac ccc gcc tgg ctt gga ggc tgg gtt gcg ata acc gca gtc gtg gca 883
 Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile Thr Ala Val Val Ala
 250 255 260

tgt gtt ttc gca gca ctt ttc agc cgc cgc tta tca cga agt ttc ggt 931
 Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu Ser Arg Ser Phe Gly
 265 270 275

gga ctc aac gga gac tgc atc ggc gca tgc att cat ctc ggg gcg tcg 979
 Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile His Leu Gly Ala Ser
 280 285 290

att tct gca gtg atg ttt gct gtt gtc gcc aat gca atg gtg
 1021
 Ile Ser Ala Val Met Phe Ala Val Val Ala Asn Ala Met Val
 295 300 305

taaagcgggtg gcgtcttttg gga
 1044

<210> 834

<211> 307

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 834

Met Ser Gly Lys Ala Gly Phe Thr Pro Glu Asp Pro Glu Asp Ser Asp
 1 5 10 15

Asn Arg His Gly Asn Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn
 20 25 30
 Trp Met Thr Val Leu Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr
 35 40 45
 Thr Gly Ala Arg Val Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe
 50 55 60
 Gly Met Phe Thr Ala Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly
 65 70 75 80
 Val Ile His Val Asp Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe
 85 90 95
 Trp Glu Leu Leu Asn Arg Phe Met His Leu Asp Gly Leu Ala Asp Val
 100 105 110
 Ser Asp Ala Leu Gly Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile
 115 120 125
 Leu Ala Asp Pro Arg Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu
 130 135 140
 Ser Val Leu Leu Gln Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr
 145 150 155 160
 Val Trp Trp Met Ile Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly
 165 170 175
 Gln Val Thr Ala Leu Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe
 180 185 190
 Gly Ala Leu Val Ile Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp
 195 200 205
 Leu Leu Val Thr Ala Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser
 210 215 220
 Pro Leu Ser Pro Leu Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro
 225 230 235 240
 Phe Pro Ala Ala Ile Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile
 245 250 255
 Thr Ala Val Val Ala Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu
 260 265 270
 Ser Arg Ser Phe Gly Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile
 275 280 285
 His Leu Gly Ala Ser Ile Ser Ala Val Met Phe Ala Val Val Ala Asn
 290 295 300
 Ala Met Val
 305

<210> 835

<211> 1197

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1174)

<223> RXA02135

<400> 835

```

cgtgtcgcag cgatttgcga gaggggtgtc ttcgtggttg ctggtctgcc actagagttg 60

aaaacgtttt aagaaaacag tcggtttgaa ggagttgtta atg gtt cca gca gag 115
                                         Met Val Pro Ala Glu
                                         1           5

ctt ttt gcg cgt gtg gaa ttt ccg gat cat aaa atc ctg gct cag acg 163
Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys Ile Leu Ala Gln Thr
          10           15           20

aag gat ttc cat gac tcc ctc acc aag cca ccc gga tct ttg ggc aag 211
Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro Gly Ser Leu Gly Lys
          25           30           35

ttg gag cag atc ggc tgt ttc att tcc gca tgc cag ggc cag att ccg 259
Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys Gln Gly Gln Ile Pro
          40           45           50

cca cgt cca ctc aac aac tca aag atc gtt gtt ttc gct ggc gat cac 307
Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val Phe Ala Gly Asp His
          55           60           65

ggc gtt gca act aaa ggc gtg tcc gcg tac cca tcc tca gta agc ttg 355
Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu
          70           75           80           85

cag atg gct gaa aac att aca aac ggt ggc gcc gcc atc aac gtg att 403
Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala Ala Ile Asn Val Ile
          90           95           100

gca cgc acc acc ggc acg tcc gtc cga ctt att gat acc tcc ctc gac 451
Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp
          105           110           115

cac gaa gca tgg ggc gac gag cgc gta tct agg tcc tgc gga tcc atc 499
His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg Ser Cys Gly Ser Ile
          120           125           130

gat gtt gaa gac gcc atg acc caa gaa cag gtc gaa cgc gca ctg aag 547
Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val Glu Arg Ala Leu Lys
          135           140           145

atc ggt aag cgc att gcg gat caa gaa gtg gac gca ggc gcc gac att 595
Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp Ala Gly Ala Asp Ile
          150           155           160           165

tta atc ccc ggc gat tta gga att ggc aac acc acc acc gcc gct gcc 643
Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala
          170           175           180

ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc 691
Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val Val Val Val Gly Arg

```

185	190	195	
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc			739
Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile			
200	205	210	
cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc			787
Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala			
215	220	225	
atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc			835
Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe			
230	235	240	245
att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac ggc gtt			883
Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val			
250	255	260	
gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc			931
Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala			
265	270	275	
agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc			979
Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser			
280	285	290	
gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg			
1027			
Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met			
295	300	305	
tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag			
1075			
Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys			
310	315	320	325
att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc ggc			
1123			
Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly			
330	335	340	
gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg			
1171			
Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr			
345	350	355	
gag taactttcta agcgatgtcc ggc			
1197			
Glu			

<210> 836

<211> 358

<212> PRT

<213> Corynebacterium glutamicum

<400> 836

Met Val Pro Ala Glu Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys

1

5

10

15

Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro
 20 25 30
 Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys
 35 40 45
 Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val
 50 55 60
 Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro
 65 70 75 80
 Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala
 85 90 95
 Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile
 100 105 110
 Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg
 115 120 125
 Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val
 130 135 140
 Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp
 145 150 155 160
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr
 165 170 175
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val
 180 185 190
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu
 195 200 205
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg
 210 215 220
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala
 225 230 235 240
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val
 245 250 255
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys
 260 265 270
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr
 275 280 285
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile
 290 295 300
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala
 305 310 315 320
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr
 325 330 335
 Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala

340

345

350

Pro Glu Gln Asn Thr Glu
355

<210> 837

<211> 645

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(622)

<223> RXA02136

<400> 837

tggttttggt ctgggttact acgcgtattc ccgcaccatt cagcctcgta agtggcggtac 60

ccctcggtgca cgcgttgaaa ttggtgctga agtctagcgc atg cgc acg tta gtt 115
Met Arg Thr Leu Val
1 5

ctt ggc ggg gcc agg tct ggt aag tct gct ttt gca gaa tca ctt gtt 163
Leu Gly Gly Ala Arg Ser Gly Lys Ser Ala Phe Ala Glu Ser Leu Val
10 15 20

gga tct ggt ccc gtt ttg tat gtc gca acg gca agg cct tcg gga gat 211
Gly Ser Gly Pro Val Leu Tyr Val Ala Thr Ala Arg Pro Ser Gly Asp
25 30 35

gat cct gaa ttc gcc gag cgc att gcg gtt cat gcg gag cgg cgc cca 259
Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His Ala Glu Arg Arg Pro
40 45 50

acg tct tgg gtg ttg gac gag gag ggg gac gtc gat aag ctt ctt gcc 307
Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val Asp Lys Leu Leu Ala
55 60 65

tcg cca ccg gcc atg ccg gtg ctc gtt gat gac ctg ggc acc tgg ctc 355
Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp Leu Gly Thr Trp Leu
70 75 80 85

acg cac gcc acc gat gcg tgc gac ggt tgg gag gcg agt tcg gcg cag 403
Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu Ala Ser Ser Ala Gln
90 95 100

ctt gag gcc aag atg gat ttg ctt atc gac gcc atc ctc cac ttt cag 451
Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala Ile Leu His Phe Gln
105 110 115

ggc gaa gat ctg gta att gtt tca cct gaa gtt ggt atg gga atc gtc 499
Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val Gly Met Gly Ile Val
120 125 130

ccg gaa tat aaa tct ggg cgc ctt ttt cgt gat cgc atc ggc aca ctt 547
Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp Arg Ile Gly Thr Leu
135 140 145

aat cag cgt gtc gca gcg att tgc gag agg gtt gtc ttc gtg gtt gct 595
Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val Val Phe Val Val Ala

150 155 160 165 642

ggt ctg cca cta gag ttg aaa acg ttt taagaaaaca gtcggtttga
Gly Leu Pro Leu Glu Leu Lys Thr Phe

170

agg 645

```
<210> 838
<211> 174
<212> PRT
<213> Corynebacterium glutamicum
```

```
<400> 838
Met Arg Thr Leu Val Leu Gly Gly Ala Arg Ser Gly Lys Ser Ala Phe
  1             5             10            15
```

Ala Glu Ser Leu Val Gly Ser Gly Pro Val Leu Tyr Val Ala Thr Ala
20 25 30

Arg Pro Ser Gly Asp Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His
35 40 45

Ala Glu Arg Arg Pro Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val
50 55 60

Asp Lys Leu Leu Ala Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp
65 70 75 80

Leu Gly Thr Trp Leu Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu
85 90 95

Ala Ser Ser Ala Gln Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala
100 105 110

Ile Leu His Phe Gln Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val
115 120 125

Gly Met Gly Ile Val Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp
130 135 140

Arg Ile Gly Thr Leu Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val
145 150 155 160

Val Phe Val Val Ala Gly Leu Pro Leu Glu Leu Lys Thr Phe
165 170

```
<210> 839
<211> 575
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (1)..(552)  
<223> RXN03114
```

<400> 839
act ccg qgg cat ttt gtt gcg ctc gcg cgg gag att gcg ggc gcg gtg 48

Thr Pro Gly His Phe Val Ala Leu Ala Arg Glu Ile Ala Gly Ala Val
 1 5 10 15
 cgc cgc gag ttg acg gtg ggg ttg gat gct ggt gac ggt ccg att tta 96
 Arg Arg Glu Leu Thr Val Gly Leu Asp Ala Gly Asp Gly Pro Ile Leu
 20 25 30
 agg cag agc ttt gat gtt ggt ttt ttg ctt gtc gac gcc tcc ttc cac 144
 Arg Gln Ser Phe Asp Val Gly Phe Leu Leu Val Asp Ala Ser Phe His
 35 40 45
 att cat atc aat ggc gtg tct act ggg cag tcg gtt gcg ccg gat gat 192
 Ile His Ile Asn Gly Val Ser Thr Gly Gln Ser Val Ala Pro Asp Asp
 50 55 60
 gta gtt gag gtg gtg cgt ggt ttg gct gat gct tcg gag ttg tcc gtg 240
 Val Val Glu Val Val Arg Gly Leu Ala Asp Ala Ser Glu Leu Ser Val
 65 70 75 80
 gaa agt gtt gct gag ttg tgt act ccc gtg gca ccg gtt tca tta tct 288
 Glu Ser Val Ala Glu Leu Cys Thr Pro Val Ala Pro Val Ser Leu Ser
 85 90 95
 gag gca cag ggg aat cct gcg cct att ggg tgg ttg gag cat gat ggc 336
 Glu Ala Gln Gly Asn Pro Ala Pro Ile Gly Trp Leu Glu His Asp Gly
 100 105 110
 gtg gtg tcg ttg ggt gcg ggt att cca ggg ggg cgg gtg gag gct cgt 384
 Val Val Ser Leu Gly Ala Gly Ile Pro Gly Gly Arg Val Glu Ala Arg
 115 120 125
 tta gcg cgt ttt att gcg gtg att gag gcg gag acc act att acc cca 432
 Leu Ala Arg Phe Ile Ala Val Ile Glu Ala Glu Thr Thr Ile Thr Pro
 130 135 140
 tgg aat tcg ttg atc att cat gat ttg tat gag ggt gtt gca gaa cag 480
 Trp Asn Ser Leu Ile Ile His Asp Leu Tyr Glu Gly Val Ala Glu Gln
 145 150 155 160
 gtg gtg aag gtt ctg gct ccc atg ggg ttg gtt ttt gat gct aat tca 528
 Val Val Lys Val Leu Ala Pro Met Gly Leu Val Phe Asp Ala Asn Ser
 165 170 175
 ccg ctt ctg gag tca ccg gct ttg taactcgcca ttggtgcacg tct 575
 Pro Leu Leu Glu Ser Pro Ala Leu
 180

<210> 840

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 840

Thr Pro Gly His Phe Val Ala Leu Ala Arg Glu Ile Ala Gly Ala Val
 1 5 10 15
 Arg Arg Glu Leu Thr Val Gly Leu Asp Ala Gly Asp Gly Pro Ile Leu
 20 25 30
 Arg Gln Ser Phe Asp Val Gly Phe Leu Leu Val Asp Ala Ser Phe His

[illegible]

```
<210> 841
<211> 1200
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1177)
<223> RXN01810
```

<400> 841															60	
ccaccaccac	aatgttgctc	atcctcgcg	cggttcgtt	gtgcgcaggt	ggctccatg	actgactc										
gcttcaccgt	cggcaaccgc	actggaaaat	aaggcttcac	atg	aat	aac	gct	ttt							115	
				Met	Asn	Asn	Ala	Phe								
				1				5								
cga	cgc	acc	ctt	aca	tcc	gta	gtc	ctc	gcc	gct	agc	ttg	gcc	tta	acg	163
Arg	Arg	Thr	Leu	Thr	Ser	Val	Val	Leu	Ala	Ala	Ser	Leu	Ala	Leu	Thr	
				10					15					20		
gcc	tgc	gca	agc	tgg	gat	tca	cct	acg	gca	tct	tcc	aat	ggt	gat	ctg	211
Ala	Cys	Ala	Ser	Trp	Asp	Ser	Pro	Thr	Ala	Ser	Ser	Asn	Gly	Asp	Leu	
			25					30					35			
att	gag	gag	atc	cag	gca	agc	tcc	acc	tca	aca	gat	ccg	cgc	acc	ttc	259
Ile	Glu	Glu	Ile	Gln	Ala	Ser	Ser	Thr	Ser	Thr	Asp	Pro	Arg	Thr	Phe	
			40				45					50				
aca	ggc	ttg	agc	atc	gtg	gaa	gat	atc	ggc	gat	gtg	gtt	ccc	gta	acc	307
Thr	Gly	Leu	Ser	Ile	Val	Glu	Asp	Ile	Gly	Asp	Val	Val	Pro	Val	Thr	

55	60	65	
gac aac gcc tca cca gct ctg cca gtt tct ttg acc gac gct gat ggc			355
Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu Thr Asp Ala Asp Gly			
70	75	80	85
aac gac gtg gtg gtg gag aac gtg tcc cgc atc ctc cca ctg gat ctc			403
Asn Asp Val Val Val Glu Asn Val Ser Arg Ile Leu Pro Leu Asp Leu			
	90	95	100
tac gga acc tat tcc aaa acc atc gct ggc ctg gga ctc gtg gac aat			451
Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu Gly Leu Val Asp Asn			
	105	110	115
att gtg ggt cgt act gtt agt tcc acc gag cct gca ttg gcg gac att			499
Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro Ala Leu Ala Asp Ile			
	120	125	130
gag gtg gtc acc act ggc gga cac acc ctc aat gct gaa gcg atc ctt			547
Glu Val Val Thr Thr Gly Gly His Thr Leu Asn Ala Glu Ala Ile Leu			
	135	140	145
aat tta cat ccg act ttg gtg atc atc gac cac tcg atc ggc cca cgc			595
Asn Leu His Pro Thr Leu Val Ile Ile Asp His Ser Ile Gly Pro Arg			
	150	155	160
gaa gtc atc gat cag atc cgc gca gct ggt gtc gcc acg gtg atc atg			643
Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val Ala Thr Val Ile Met			
	170	175	180
tcg ccg cag cgt tcc att gcc tca att ggc gac gac atc cgc gac atc			691
Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp Asp Ile Arg Asp Ile			
	185	190	195
gcc tcc gtc gtt gga ctt cct gaa gaa ggg gag aag ctc gcg gaa cgt			739
Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu Lys Leu Ala Glu Arg			
	200	205	210
tcc gtt gct gaa gtc gaa gag gcc agc acg gtt gtc gat gaa ctc acc			787
Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val Val Asp Glu Leu Thr			
	215	220	225
cca gaa gat ccc ctc aaa atg gta ttc ctc tat gcc cgc gga act ggt			835
Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr Ala Arg Gly Thr Gly			
	230	235	240
gga gtg ttc ttc att ttg ggc gat gcc tat ggt gga cgc gat ctc att			883
Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly Gly Arg Asp Leu Ile			
	250	255	260
gaa ggc ctg ggc ggc gtc gac atg gct gct gaa aag ggc atc atg gat			931
Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu Lys Gly Ile Met Asp			
	265	270	275
ctg gca cca gcc aac gcg gaa gca ctt gcc gaa cta aat cca gac gtc			979
Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu Leu Asn Pro Asp Val			
	280	285	290
ttc gtg atg atg tcg gaa gga cta gtc tcg aca gga ggt atc gac ggt			
1027			
Phe Val Met Met Ser Glu Gly Leu Val Ser Thr Gly Gly Ile Asp Gly			

295 300 305
 ctt atg gaa cgc ccc ggc att gct cag aca acc gcc gga caa aac caa
 1075
 Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr Ala Gly Gln Asn Gln
 310 315 320 325
 cga gta ctg gcg ctt ccc gat ggt caa tca ttg gcc ttt ggt gcc caa
 1123
 Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu Ala Phe Gly Ala Gln
 330 335 340
 act ggc gag ttg ttg ctc cgc gca tcc cgc gaa ctg tat gtg cag ggc
 1171
 Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu Leu Tyr Val Gln Gly
 345 350 355
 ggc gag tagatgggtg tgaaggaggt tga
 1200
 Gly Glu

<210> 842
 <211> 359
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 842
 Met Asn Asn Ala Phe Arg Arg Thr Leu Thr Ser Val Val Leu Ala Ala
 1 5 10 15
 Ser Leu Ala Leu Thr Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser
 20 25 30
 Ser Asn Gly Asp Leu Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr
 35 40 45
 Asp Pro Arg Thr Phe Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp
 50 55 60
 Val Val Pro Val Thr Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu
 65 70 75 80
 Thr Asp Ala Asp Gly Asn Asp Val Val Val Glu Asn Val Ser Arg Ile
 85 90 95
 Leu Pro Leu Asp Leu Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu
 100 105 110
 Gly Leu Val Asp Asn Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro
 115 120 125
 Ala Leu Ala Asp Ile Glu Val Val Thr Thr Gly Gly His Thr Leu Asn
 130 135 140
 Ala Glu Ala Ile Leu Asn Leu His Pro Thr Leu Val Ile Ile Asp His
 145 150 155 160
 Ser Ile Gly Pro Arg Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val
 165 170 175

Ala Thr Val Ile Met Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp
 180 185 190

Asp Ile Arg Asp Ile Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu
 195 200 205

Lys Leu Ala Glu Arg Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val
 210 215 220

Val Asp Glu Leu Thr Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr
 225 230 235 240

Ala Arg Gly Thr Gly Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly
 245 250 255

Gly Arg Asp Leu Ile Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu
 260 265 270

Lys Gly Ile Met Asp Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu
 275 280 285

Leu Asn Pro Asp Val Phe Val Met Met Ser Glu Gly Leu Val Ser Thr
 290 295 300

Gly Gly Ile Asp Gly Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr
 305 310 315 320

Ala Gly Gln Asn Gln Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu
 325 330 335

Ala Phe Gly Ala Gln Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu
 340 345 350

Leu Tyr Val Gln Gly Gly Glu
 355

<210> 843

<211> 963

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(933)

<223> RXS03205

<400> 843

gat tcc ggc att ccc acg cag ttg gtg gag ggc agc tgg ttt gaa ccg 48
 Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1 5 10 15

gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg 96
 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30

gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat 144
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc 192
 Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
 50 55 60

aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg 240
 Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
 65 70 75 80

gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt 288
 Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95

tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat 336
 Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
 100 105 110

gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag 384
 Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu
 115 120 125

gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag 432
 Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys
 130 135 140

gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa 480
 Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
 145 150 155 160

gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag 528
 Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
 165 170 175

tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc 576
 Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190

acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc 624
 Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205

ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat 672
 Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220

gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc 720
 Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240

acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc 768
 Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255

atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg 816
 Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270

gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac 864
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285

ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg 912

Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300

ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aagccggtttt 963
 Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 844

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 844

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1 5 10 15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
 50 55 60

Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
 65 70 75 80

Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95

Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
 100 105 110

Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu
 115 120 125

Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys
 130 135 140

Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
 145 150 155 160

Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
 165 170 175

Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190

Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205

Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220

Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240

Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255

Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270

Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285

Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300

Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 845

<211> 956

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(933)

<223> FRXA00306

<400> 845

gat tcc ggc att ccc acg cag ttg gtg gag ggc agc tgg ttt gaa ccg 48
 Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1 5 10 15

gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg 96
 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30

gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat 144
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc 192
 Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
 50 55 60

aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg 240
 Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
 65 70 75 80

gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt 288
 Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95

tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat 336
 Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
 100 105 110

gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag 384
 Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu
 115 120 125

gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag 432
 Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys
 130 135 140


```

gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa 480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
145                150                155                160

gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag 528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
165                170                175

tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc 576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
180                185                190

acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc 624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
195                200                205

ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat 672
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
210                215                220

gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc 720
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
225                230                235

acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc 768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
245                250                255

atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg 816
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
260                265                270

gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac 864
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
275                280                285

ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg 912
Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
290                295                300

ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag 956
Pro Ala Asp Leu Leu Asp Ser
305                310

```

<210> 846

<211> 311

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 846

```

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1                5                10                15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
20                25                30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
35                40                45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu

```

50	55	60
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala		
65	70	75 80
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly		
	85	90 95
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr		
	100	105 110
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu		
	115	120 125
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys		
	130	135 140
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu		
	145	150 155 160
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln		
	165	170 175
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg		
	180	185 190
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg		
	195	200 205
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp		
	210	215 220
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg		
	225	230 235 240
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser		
	245	250 255
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu		
	260	265 270
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn		
	275	280 285
Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu		
	290	295 300
Pro Ala Asp Leu Leu Asp Ser		
	305	310

<210> 847

<211> 819

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(796)

<223> RXC01715

<400> 847

```

acatgttggtt ggaacatgcc ggcagagccg acactacgat tcattcgcta aaggggtctgg 60

ccactgacac tggcaaagat ccacgaaagg aagttaccct gtg agc gag ctc gat 115
                                   Val Ser Glu Leu Asp
                                   1 5

att aaa cag ctc aac aaa ctg cag cgc tac tct cag tgg gcg gtg ttc 163
Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser Gln Trp Ala Val Phe
                                   10 15 20

cgt gct att cct gga gcg ctc gat gat gat cgc aca gaa gtc act gac 211
Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg Thr Glu Val Thr Asp
                                   25 30 35

caa gca gcc aag ttc ttt gcc gac ctt gaa gca gaa ggc aaa gtc act 259
Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala Glu Gly Lys Val Thr
                                   40 45 50

gtc cgt ggc att tac aac gcc tcc ggc ctg cgc gca gac gct gac tac 307
Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg Ala Asp Ala Asp Tyr
                                   55 60 65

atg atc tgg tgg cac gca gaa gaa ttc gaa gac att cag aag gcc ttc 355
Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp Ile Gln Lys Ala Phe
                                   70 75 80 85

gct gat ttc cgc cgc acc acc att ttg ggt cag gtt tct gag gtc ttc 403
Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln Val Ser Glu Val Phe
                                   90 95 100

tgg atc gga aac gct ctc cac cgt cca tct gag ttc aac aag gct cac 451
Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu Phe Asn Lys Ala His
                                   105 110 115

ttg cct tca ttc atc atg ggt gaa gaa gca aag gac tgg atc act gtt 499
Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys Asp Trp Ile Thr Val
                                   120 125 130

tac ccg ttc gtg cgc agc tac gac tgg tac atc atg gag ccc ttg aag 547
Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile Met Glu Pro Leu Lys
                                   135 140 145

cgt tcc cgc att ctc cgc gag cac gga caa gct gct gtg gaa ttc cca 595
Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala Ala Val Glu Phe Pro
150 155 160 165

gat gtt cgt gcc aac act gtg ccg gct ttc gca ctg ggt gac tac gaa 643
Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala Leu Gly Asp Tyr Glu
                                   170 175 180

tgg gtg ctg gct ttc gag gct gat gag ttg cac cgc att gtc gat ttg 691
Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His Arg Ile Val Asp Leu
                                   185 190 195

atg cac aag atg cgt tac acc gag gct cgc ctc cac gtc cgt gag gag 739
Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu His Val Arg Glu Glu
                                   200 205 210

ctg cca ttt att tct gga cag cgc gtc gac att gca gat ctg att aag 787
Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile Ala Asp Leu Ile Lys

```

215 220 225 819
 gtt ctt cct taaaagctgc ttttctaaac gat
 Val Leu Pro
 230

<210> 848
 <211> 232
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 848
 Val Ser Glu Leu Asp Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser
 1 5 10 15
 Gln Trp Ala Val Phe Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg
 20 25 30
 Thr Glu Val Thr Asp Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala
 35 40 45
 Glu Gly Lys Val Thr Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg
 50 55 60
 Ala Asp Ala Asp Tyr Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp
 65 70 75 80
 Ile Gln Lys Ala Phe Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln
 85 90 95
 Val Ser Glu Val Phe Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu
 100 105 110
 Phe Asn Lys Ala His Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys
 115 120 125
 Asp Trp Ile Thr Val Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile
 130 135 140
 Met Glu Pro Leu Lys Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala
 145 150 155 160
 Ala Val Glu Phe Pro Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala
 165 170 175
 Leu Gly Asp Tyr Glu Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His
 180 185 190
 Arg Ile Val Asp Leu Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu
 195 200 205
 His Val Arg Glu Glu Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile
 210 215 220
 Ala Asp Leu Ile Lys Val Leu Pro
 225 230

<210> 849
 <211> 1587

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1564)

<223> RXN00420

<400> 849

attcgtgaac tcattgatct ttaggcaata aatgtgagat tggacgattt cagccttgtc 60

ttcaccacct	gaaaattttc	gggggtaacc	tttaaaggcg	atg	aac	agt	tct	cac	115
				Met	Asn	Ser	Ser	His	
				1				5	

ggc	acg	tcc	agc	tcc	ggc	gct	tcg	gcc	ggg	gcc	cac	gga	gcc	ctt	ccc	163
Gly	Thr	Ser	Ser	Ser	Gly	Ala	Ser	Ala	Gly	Ala	His	Gly	Ala	Leu	Pro	
			10						15					20		

cta	gaa	gct	cag	aaa	ctg	aac	ggg	tgg	ggc	cgc	aca	gcc	ccc	acc	acc	211
Leu	Glu	Ala	Gln	Lys	Leu	Asn	Gly	Trp	Gly	Arg	Thr	Ala	Pro	Thr	Thr	
			25					30					35			

gct	gag	gta	ctt	acc	acc	cca	gac	cta	gac	atc	att	gtg	gat	gca	gtc	259
Ala	Glu	Val	Leu	Thr	Thr	Pro	Asp	Leu	Asp	Ile	Ile	Val	Asp	Ala	Val	
		40					45					50				

cgc	caa	gtc	gct	gaa	caa	aac	gac	tcc	aag	ccg	gac	tac	ctc	aag	cgc	307
Arg	Gln	Val	Ala	Glu	Gln	Asn	Asp	Ser	Lys	Pro	Asp	Tyr	Leu	Lys	Arg	
	55					60					65					

ggc	gtg	att	gcc	cgt	ggc	atg	ggg	cgt	tcc	tat	ggg	gac	cca	gcc	caa	355
Gly	Val	Ile	Ala	Arg	Gly	Met	Gly	Arg	Ser	Tyr	Gly	Asp	Pro	Ala	Gln	
	70				75					80					85	

aac	gcc	ggg	ggc	ctt	gtc	att	gac	atg	cag	cca	ctg	aac	aaa	atc	cac	403
Asn	Ala	Gly	Gly	Leu	Val	Ile	Asp	Met	Gln	Pro	Leu	Asn	Lys	Ile	His	
			90						95					100		

tcg	att	gat	cct	gat	tct	gcg	atc	gtc	gat	gta	gat	ggc	ggc	gtc	acc	451
Ser	Ile	Asp	Pro	Asp	Ser	Ala	Ile	Val	Asp	Val	Asp	Gly	Gly	Val	Thr	
			105					110					115			

ctc	gat	cag	ctc	atg	aag	gct	gcc	ctg	cca	tat	ggc	ctc	tgg	gtt	cct	499
Leu	Asp	Gln	Leu	Met	Lys	Ala	Ala	Leu	Pro	Tyr	Gly	Leu	Trp	Val	Pro	
		120					125					130				

gtc	ctt	ccc	ggc	acc	cgc	caa	gtc	acc	atc	ggg	ggc	gca	atc	gga	cca	547
Val	Leu	Pro	Gly	Thr	Arg	Gln	Val	Thr	Ile	Gly	Gly	Ala	Ile	Gly	Pro	
	135					140					145					

gac	atc	cac	ggg	aag	aac	cac	cac	tct	gca	ggg	tcc	ttc	ggc	gac	cac	595
Asp	Ile	His	Gly	Lys	Asn	His	His	Ser	Ala	Gly	Ser	Phe	Gly	Asp	His	
	150				155				160					165		

gtg	gtc	tcc	atg	gaa	ctc	ctc	gtt	gca	gac	gga	cgc	atc	ctg	cac	ctc	643
Val	Val	Ser	Met	Glu	Leu	Leu	Val	Ala	Asp	Gly	Arg	Ile	Leu	His	Leu	
				170				175					180			

gag	cca	gaa	ggc	acc	gcc	gaa	gac	cca	cag	ggc	gac	ctg	ttc	tgg	gca	691
Glu	Pro	Glu	Gly	Thr	Ala	Glu	Asp	Pro	Gln	Gly	Asp	Leu	Phe	Trp	Ala	

185	190	195	
acc gtt ggt ggc atg ggc ctg acc ggc atc atc gtc cgt gca cgc atc			739
Thr Val Gly Gly Met Gly Leu Thr Gly Ile Ile Val Arg Ala Arg Ile			
200	205	210	
cgc atg acc aag acg gaa acc gcc tac ttc att gcg gac acc gac cgc			787
Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile Ala Asp Thr Asp Arg			
215	220	225	
acc aac aac ttg gaa gaa acc gtt gcg ttc cac tcc gac gga tca gag			835
Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His Ser Asp Gly Ser Glu			
230	235	240	245
cac aac tac acc tat tct tct gcg tgg ttc gat gtc atc agc cct gag			883
His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp Val Ile Ser Pro Glu			
250	255	260	
cca aag ctt ggc cgc tcc acc atc tcc cgt ggt tcc ctg gca aca ctt			931
Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly Ser Leu Ala Thr Leu			
265	270	275	
gct cag ctg gaa gaa ttg gca cca aag ctg gcc aag gat cca ctg aag			979
Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala Lys Asp Pro Leu Lys			
280	285	290	
ttt aat gct cca cag ctg atg aag gtt cca gat atc ttc cca tcc tgg			
1027			
Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp Ile Phe Pro Ser Trp			
295	300	305	
act ttg aac aag ctg acc ctt tcc gca gtc ggt gtg gct tac tac gcc			
1075			
Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr Ala			
310	315	320	325
atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc tac			
1123			
Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe Tyr			
330	335	340	
caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc aag			
1171			
Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser Lys			
345	350	355	
ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag cct			
1219			
Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu Pro			
360	365	370	
ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc gca			
1267			
Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser Ala			
375	380	385	
ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg tcc			
1315			
Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu Ser			
390	395	400	405

tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc cca
1363

Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg Pro
410 415 420

ggc ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa ttc
1411

Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu Phe
425 430 435

ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag aac
1459

Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu Asn
440 445 450

ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga aat
1507

Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg Asn
455 460 465

gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga ctt
1555

Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg Leu
470 475 480 485

gag ctt tct taagaaaggg cttgaactaa aca
1587

Glu Leu Ser

<210> 850

<211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 850

Met Asn Ser Ser His Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala
1 5 10 15

His Gly Ala Leu Pro Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg
20 25 30

Thr Ala Pro Thr Thr Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile
35 40 45

Ile Val Asp Ala Val Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro
50 55 60

Asp Tyr Leu Lys Arg Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr
65 70 75 80

Gly Asp Pro Ala Gln Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro
85 90 95

Leu Asn Lys Ile His Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val
100 105 110

Asp Gly Gly Val Thr Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr
115 120 125

Gly Leu Trp Val Pro Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly
 130 135 140
 Gly Ala Ile Gly Pro Asp Ile His Gly Lys Asn His His Ser Ala Gly
 145 150 155 160
 Ser Phe Gly Asp His Val Val Ser Met Glu Leu Leu Val Ala Asp Gly
 165 170 175
 Arg Ile Leu His Leu Glu Pro Glu Gly Thr Ala Glu Asp Pro Gln Gly
 180 185 190
 Asp Leu Phe Trp Ala Thr Val Gly Gly Met Gly Leu Thr Gly Ile Ile
 195 200 205
 Val Arg Ala Arg Ile Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile
 210 215 220
 Ala Asp Thr Asp Arg Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His
 225 230 235 240
 Ser Asp Gly Ser Glu His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp
 245 250 255
 Val Ile Ser Pro Glu Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly
 260 265 270
 Ser Leu Ala Thr Leu Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala
 275 280 285
 Lys Asp Pro Leu Lys Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp
 290 295 300
 Ile Phe Pro Ser Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly
 305 310 315 320
 Val Ala Tyr Tyr Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn
 325 330 335
 Leu Thr Gln Phe Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg
 340 345 350
 Gly Tyr Gly Ser Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr
 355 360 365
 Glu Ala Val Glu Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser
 370 375 380
 Gly His Tyr Ser Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn
 385 390 395 400
 Arg Ala Pro Leu Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp
 405 410 415
 Phe Pro Ile Arg Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys
 420 425 430
 Arg Val Met Glu Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg
 435 440 445
 Thr Ser Ala Glu Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp

450 455 460

Leu Lys Thr Arg Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp
 465 470 475 480

Met Ser Arg Arg Leu Glu Leu Ser
 485

<210> 851
 <211> 563
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(540)
 <223> FRXA00420

<400> 851

tgg act ttg aac aag ctg acc ctt tcc gca gtc ggt gtg gct tac tac	48
Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr	
1 5 10 15	
gcc atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc	96
Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe	
20 25 30	
tac caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc	144
Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser	
35 40 45	
aag ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag	192
Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu	
50 55 60	
cct ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc	240
Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser	
65 70 75 80	
gca ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg	288
Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu	
85 90 95	

tcc tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc	336
Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg	
100 105 110	
cca ggt ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa	384
Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu	
115 120 125	
ttc ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag	432
Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu	
130 135 140	
aac ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga	480
Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg	
145 150 155 160	
aat gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga	528

Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg
 165 170 175

ctt gag ctt tct taagaaaggg cttgaactaa aca 563
 Leu Glu Leu Ser
 180

<210> 852

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 852

Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr
 1 5 10 15

Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe
 20 25 30

Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser
 35 40 45

Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu
 50 55 60

Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser
 65 70 75 80

Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu
 85 90 95

Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg
 100 105 110

Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu
 115 120 125

Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu
 130 135 140

Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg
 145 150 155 160

Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg
 165 170 175

Leu Glu Leu Ser
 180

<210> 853

<211> 622

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(622)

<223> FRXA00426

<400> 853

attcgtgaac tcattggatct ttaggcaata aatgtgagat tggacgattt cacgcttgtc 60

ttcaccacct gaaaattttc gggggtaacc tttaaaggcg atg aac agt tct cac 115
 Met Asn Ser Ser His
 1 5

ggc acg tcc agc tcc ggc gct tcg gcc ggt gcc cac gga gcc ctt ccc 163
 Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala His Gly Ala Leu Pro
 10 15 20

cta gaa gct cag aaa ctg aac ggt tgg ggc cgc aca gcc ccc acc acc 211
 Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg Thr Ala Pro Thr Thr
 25 30 35

gct gag gta ctt acc acc cca gac cta gac atc att gtg gat gca gtc 259
 Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile Ile Val Asp Ala Val
 40 45 50

cgc caa gtc gct gaa caa aac gac tcc aag ccg gac tac ctc aag cgc 307
 Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro Asp Tyr Leu Lys Arg
 55 60 65

ggc gtg att gcc cgt ggc atg ggt cgt tcc tat ggt gac cca gcc caa 355
 Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr Gly Asp Pro Ala Gln
 70 75 80 85

aac gcc ggt ggc ctt gtc att gac atg cag cca ctg aac aaa atc cac 403
 Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro Leu Asn Lys Ile His
 90 95 100

tcg att gat cct gat tct gcg atc gtc gat gta gat ggc ggc gtc acc 451
 Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val Asp Gly Gly Val Thr
 105 110 115

ctc gat cag ctc atg aag gct gcc ctg cca tat ggc ctc tgg gtt cct 499
 Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr Gly Leu Trp Val Pro
 120 125 130

gtc ctt ccc ggc acc cgc caa gtc acc atc ggt ggc gca atc gga cca 547
 Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly Gly Ala Ile Gly Pro
 135 140 145

gac atc cac ggt aag aac cac cac tct gca ggt tcc ttc ggc gac cac 595
 Asp Ile His Gly Lys Asn His His Ser Ala Gly Ser Phe Gly Asp His
 150 155 160 165

gtg gtc tcc atg gaa ctc ctc gtt gca 622
 Val Val Ser Met Glu Leu Leu Val Ala
 170

<210> 854

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 854

Met Asn Ser Ser His Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala
 1 5 10 15

His	Gly	Ala	Leu	Pro	Leu	Glu	Ala	Gln	Lys	Leu	Asn	Gly	Trp	Gly	Arg	
			20						25						30	
Thr	Ala	Pro	Thr	Thr	Ala	Glu	Val	Leu	Thr	Thr	Pro	Asp	Leu	Asp	Ile	
			35						40						45	
Ile	Val	Asp	Ala	Val	Arg	Gln	Val	Ala	Glu	Gln	Asn	Asp	Ser	Lys	Pro	
			50						55						60	
Asp	Tyr	Leu	Lys	Arg	Gly	Val	Ile	Ala	Arg	Gly	Met	Gly	Arg	Ser	Tyr	
			65						70						75	
Gly	Asp	Pro	Ala	Gln	Asn	Ala	Gly	Gly	Leu	Val	Ile	Asp	Met	Gln	Pro	
			85						90						95	
Leu	Asn	Lys	Ile	His	Ser	Ile	Asp	Pro	Asp	Ser	Ala	Ile	Val	Asp	Val	
			100						105						110	
Asp	Gly	Gly	Val	Thr	Leu	Asp	Gln	Leu	Met	Lys	Ala	Ala	Leu	Pro	Tyr	
			115						120						125	
Gly	Leu	Trp	Val	Pro	Val	Leu	Pro	Gly	Thr	Arg	Gln	Val	Thr	Ile	Gly	
			130						135						140	
Gly	Ala	Ile	Gly	Pro	Asp	Ile	His	Gly	Lys	Asn	His	His	Ser	Ala	Gly	
			145						150						155	
Ser	Phe	Gly	Asp	His	Val	Val	Ser	Met	Glu	Leu	Leu	Val	Ala			
			165						170							

```
<210> 855
<211> 930
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(907)
<223> RXN00708
```

<400> 855																	
cctgcgtatc	ggctgccttt	ttgaattctt	ttctcctcgc	aggcctaacc	ttcaattcct											60	
taccgatacc	cttccttgaa	gtttcgctaa	cctggcgtac	atg	act	ctt	tcc	ctt								115	
				Met	Thr	Leu	Ser	Leu									
				1								5					
cct	cca	att	ggt	ttc	ggc	acc	gtt	cat	ctt	gat	ggc	gca	cct	ggc	gtt	163	
Pro	Pro	Ile	Gly	Phe	Gly	Thr	Val	His	Leu	Asp	Gly	Ala	Pro	Gly	Val		
				10								15				20	
gaa	gcc	atc	gct	act	gcc	att	gat	gct	ggt	tac	cgc	ctc	atc	gac	acc	211	
Glu	Ala	Ile	Ala	Thr	Ala	Ile	Asp	Ala	Gly	Tyr	Arg	Leu	Ile	Asp	Thr		
				25								30				35	
gcg	tac	aac	tat	gaa	aat	gaa	ggt	acc	gtg	ggc	aag	gct	gtc	cgc	gag	259	
Ala	Tyr	Asn	Tyr	Glu	Asn	Glu	Gly	Thr	Val	Gly	Lys	Ala	Val	Arg	Glu		
				40								45				50	
tcg	ggt	gtc	ccc	cgc	gag	gaa	ttg	att	gtt	acc	agt	aag	ctc	cct	ggc	307	

Ser	Gly	Val	Pro	Arg	Glu	Glu	Leu	Ile	Val	Thr	Ser	Lys	Leu	Pro	Gly		
55						60					65						
cgc	ttc	cat	gct	cgc	gat	cta	gga	cgc	gtc	cgc	att	gag	gaa	agt	cta	355	
Arg	Phe	His	Ala	Arg	Asp	Leu	Gly	Arg	Val	Arg	Ile	Glu	Glu	Ser	Leu		
70					75					80					85		
tac	cgc	ctc	aac	tta	gat	tac	atc	gat	ctc	ctc	ttg	att	cac	tgg	cct	403	
Tyr	Arg	Leu	Asn	Leu	Asp	Tyr	Ile	Asp	Leu	Leu	Leu	Ile	His	Trp	Pro		
				90					95						100		
aat	ccc	agc	aag	gat	ctc	tac	gtc	gag	gcg	tgg	gaa	acg	ctg	att	gaa	451	
Asn	Pro	Ser	Lys	Asp	Leu	Tyr	Val	Glu	Ala	Trp	Glu	Thr	Leu	Ile	Glu		
			105					110							115		
gtc	cgc	gat	gct	ggc	ctg	gtc	aag	cac	atc	gga	gtg	tct	aac	ttc	ctt	499	
Val	Arg	Asp	Ala	Gly	Leu	Val	Lys	His	Ile	Gly	Val	Ser	Asn	Phe	Leu		
			120					125							130		
cca	aat	cac	att	gat	cgc	ctg	cgc	cgc	gaa	acc	ggt	gaa	ctg	ccg	gcc	547	
Pro	Asn	His	Ile	Asp	Arg	Leu	Arg	Arg	Glu	Thr	Gly	Glu	Leu	Pro	Ala		
			135				140								145		
gtt	aac	cag	atc	gag	ttg	cac	ccc	tat	ttc	ccg	cag	gtg	gag	cag	gta	595	
Val	Asn	Gln	Ile	Glu	Leu	His	Pro	Tyr	Phe	Pro	Gln	Val	Glu	Gln	Val		
					155					160					165		
gat	ttc	cac	gat	gag	ctg	ggc	atc	att	acc	gag	gcc	tgg	agc	ccg	ctc	643	
Asp	Phe	His	Asp	Glu	Leu	Gly	Ile	Ile	Thr	Glu	Ala	Trp	Ser	Pro	Leu		
				170					175						180		
agc	aac	ggt	cgc	gga	ctc	gtc	gaa	gag	cca	ttg	ctc	aag	gaa	atc	ggc	691	
Ser	Asn	Gly	Arg	Gly	Leu	Val	Glu	Glu	Pro	Leu	Leu	Lys	Glu	Ile	Gly		
			185					190							195		
gag	cgc	tac	ggg	gtc	ggc	agc	ggc	gaa	atc	gcc	ctc	gct	tgg	cat	cac	739	
Glu	Arg	Tyr	Gly	Val	Gly	Ser	Gly	Glu	Ile	Ala	Leu	Ala	Trp	His	His		
			200				205						210				
gcc	agg	gga	atc	gtt	ccg	att	cca	cgc	tcc	acc	aac	ccg	gcc	agg	cag	787	
Ala	Arg	Gly	Ile	Val	Pro	Ile	Pro	Arg	Ser	Thr	Asn	Pro	Ala	Arg	Gln		
			215				220								225		
cgc	agc	aac	ttg	gag	gcg	gta	aag	att	tcg	ctt	atc	gac	gaa	gac	gtc	835	
Arg	Ser	Asn	Leu	Glu	Ala	Val	Lys	Ile	Ser	Leu	Ile	Asp	Glu	Asp	Val		
230					235					240					245		
cag	gcg	att	acc	gct	ttg	gcg	cgc	aaa	aac	ggc	cgg	atc	aaa	gat	caa	883	
Gln	Ala	Ile	Thr	Ala	Leu	Ala	Arg	Lys	Asn	Gly	Arg	Ile	Lys	Asp	Gln		
				250					255						260		
gat	cca	gcc	gtc	tat	gaa	gaa	ttc	tagatagtta	catcaagggtt	ccg						930	
Asp	Pro	Ala	Val	Tyr	Glu	Glu	Phe										
			265														
<210>	856																
<211>	269																
<212>	PRT																
<213>	Corynebacterium glutamicum																

<400> 856

Met Thr Leu Ser Leu Pro Pro Ile Gly Phe Gly Thr Val His Leu Asp
 1 5 10 15

Gly Ala Pro Gly Val Glu Ala Ile Ala Thr Ala Ile Asp Ala Gly Tyr
 20 25 30

Arg Leu Ile Asp Thr Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly
 35 40 45

Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu Ile Val Thr
 50 55 60

Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly Arg Val Arg
 65 70 75 80

Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile Asp Leu Leu
 85 90 95

Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val Glu Ala Trp
 100 105 110

Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys His Ile Gly
 115 120 125

Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg Arg Glu Thr
 130 135 140

Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro Tyr Phe Pro
 145 150 155 160

Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile Ile Thr Glu
 165 170 175

Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu Glu Pro Leu
 180 185 190

Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly Glu Ile Ala
 195 200 205

Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro Arg Ser Thr
 210 215 220

Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys Ile Ser Leu
 225 230 235 240

Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg Lys Asn Gly
 245 250 255

Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
 260 265

<210> 857

<211> 695

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(672)

<223> FRXA00708

<400> 857

acc gtc ggc aag gct gtc cgc gag tcg ggt gtc ccc cgc gag gaa ttg	48
Thr Val Gly Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu	
1 5 10 15	
att gtt acc agt aag ctc cct ggc cgc ttc cat gct cgc gat cta gga	96
Ile Val Thr Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly	
20 25 30	
cgc gtc cgc att gag gaa agt cta tac cgc ctc aac tta gat tac atc	144
Arg Val Arg Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile	
35 40 45	
gat ctc ctc ttg att cac tgg cct aat ccc agc aag gat ctc tac gtc	192
Asp Leu Leu Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val	
50 55 60	
gag gcg tgg gaa acg ctg att gaa gtc cgc gat gct ggc ctg gtc aag	240
Glu Ala Trp Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys	
65 70 75 80	
cac atc gga gtg tct aac ttc ctt cca aat cac att gat cgc ctg cgc	288
His Ile Gly Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg	
85 90 95	
cgc gaa acc ggt gaa ctg ccg gcc gtt aac cag atc gag ttg cac ccc	336
Arg Glu Thr Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro	
100 105 110	
tat ttc ccg cag gtg gag cag gta gat ttc cac gat gag ctg ggc atc	384
Tyr Phe Pro Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile	
115 120 125	
att acc gag gcc tgg agc ccg ctc agc aac ggt cgc gga ctc gtc gaa	432
Ile Thr Glu Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu	
130 135 140	
gag cca ttg ctc aag gaa atc ggc gag cgc tac ggg gtc ggc agc ggc	480
Glu Pro Leu Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly	
145 150 155 160	
gaa atc gcc ctc gct tgg cat cac gcc agg gga atc gtt ccg att cca	528
Glu Ile Ala Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro	
165 170 175	
cgc tcc acc aac ccg gcc agg cag cgc agc aac ttg gag gcg gta aag	576
Arg Ser Thr Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys	
180 185 190	
att tcg ctt atc gac gaa gac gtc cag gcg att acc gct ttg gcg cgc	624
Ile Ser Leu Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg	
195 200 205	
aaa aac ggc cgg atc aaa gat caa gat cca gcc gtc tat gaa gaa ttc	672
Lys Asn Gly Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe	
210 215 220	
tagatagtta catcaagggtt ccg	695

<210> 858

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 858

Thr Val Gly Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu
 1 5 10 15

Ile Val Thr Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly
 20 25 30

Arg Val Arg Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile
 35 40 45

Asp Leu Leu Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val
 50 55 60

Glu Ala Trp Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys
 65 70 75 80

His Ile Gly Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg
 85 90 95

Arg Glu Thr Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro
 100 105 110

Tyr Phe Pro Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile
 115 120 125

Ile Thr Glu Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu
 130 135 140

Glu Pro Leu Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly
 145 150 155 160

Glu Ile Ala Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro
 165 170 175

Arg Ser Thr Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys
 180 185 190

Ile Ser Leu Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg
 195 200 205

Lys Asn Gly Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
 210 215 220

<210> 859

<211> 1038

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1015)

<223> RXA02373

<400> 859

```

aaagtcataag ctcatggtaa ttcagtgtag ataggcgtag ggtgggctat ccaattcatc 60
tcaacctaag gcgcattttg gtgcgcatca aggagaaaat atg tct gtt gtg ggt 115
Met Ser Val Val Gly
1 5
acc ggc cta ttc ttt gga tcc ccg gag gaa gag cgg gat aag ttg atg 163
Thr Gly Leu Phe Phe Gly Ser Pro Glu Glu Glu Arg Asp Lys Leu Met
10 15 20
caa tct ttg atg gat cag aag aat aag ctt tcg aag tct gaa ggt atc 211
Gln Ser Leu Met Asp Gln Lys Asn Lys Leu Ser Lys Ser Glu Gly Ile
25 30 35
cca ttg gtc acc ttg aat gat gga aaa acc att cct cag ctt ggt ttt 259
Pro Leu Val Thr Leu Asn Asp Gly Lys Thr Ile Pro Gln Leu Gly Phe
40 45 50
ggt gtg ttc aag gta gat ccc gat gaa gca gag cgc gta gtt acc gaa 307
Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu Arg Val Val Thr Glu
55 60 65
gca ctt gag gta ggt tac cgc cac atc gat act gct gcg att tac ggc 355
Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr Ala Ala Ile Tyr Gly
70 75 80 85
aat gag gaa ggt gtc ggc cga gct att gct aag tcc ggc att cct cgt 403
Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys Ser Gly Ile Pro Arg
90 95 100
gaa gag ctg ttt att act acc aag ttg tgg aac gat cgc cac ctg gat 451
Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn Asp Arg His Leu Asp
105 110 115
gta gaa gct gct ttt gag gag tct ctg cag aag ctg ggc ttg gat tat 499
Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys Leu Gly Leu Asp Tyr
120 125 130
gta gat ctg tac ttg gtg cac tgg ccg gca ccg aag aac gat aat tat 547
Val Asp Leu Tyr Leu Val His Trp Pro Ala Pro Lys Asn Asn Asn Tyr
135 140 145
ggt gct gca tgg aag ggc ttg gaa aag ctc ggt gac cgt gct cgt tcc 595
Val Ala Ala Trp Lys Gly Leu Glu Lys Leu Gly Asp Arg Ala Arg Ser
150 155 160 165
atc ggt gtg tgc aac ttc ctg cca gag cac cta gaa aag ctg ctg gca 643
Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu Glu Lys Leu Leu Ala
170 175 180
gag gca acc act gtg cct gcc att aac cag att gag ctg cac cca gct 691
Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile Glu Leu His Pro Ala
185 190 195
ttg cag cag cgc gat gct gtt gag gca tct ctt gca gca ggc atc act 739
Leu Gln Gln Arg Asp Ala Val Glu Ala Ser Leu Ala Ala Gly Ile Thr
200 205 210

```

gtg gag tcg tgg ggt cct ctg gga cag ggg cgt ttt gat ctt ggc gct 787
 Val Glu Ser Trp Gly Pro Leu Gly Gln Gly Arg Phe Asp Leu Gly Ala
 215 220 225

gag gaa cca atc gca gct gca gcg aag aac cat gga aag acc cca gct 835
 Glu Glu Pro Ile Ala Ala Ala Lys Asn His Gly Lys Thr Pro Ala
 230 235 240 245

cag gtt gtt atc cgt tgg cac ctg cag aac ggt ttc gtt gtg ttc ccc 883
 Gln Val Val Ile Arg Trp His Leu Gln Asn Gly Phe Val Val Phe Pro
 250 255 260

aag act gtg act aag agc cgc atg gtg gaa aac atc gac gtg ttt gat 931
 Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn Ile Asp Val Phe Asp
 265 270 275

ttc gaa ctc agt gat gag gag atg gct gcg atc act gct ctt gag cgc 979
 Phe Glu Leu Ser Asp Glu Glu Met Ala Ala Ile Thr Ala Leu Glu Arg
 280 285 290

aat gat cgt ggt ggt tca cac ccg aat gat ctg aac tagaaataag
 1025
 Asn Asp Arg Gly Gly Ser His Pro Asn Asp Leu Asn
 295 300 305

gtaaggccct gca
 1038

<210> 860

<211> 305

<212> PRT

<213> Corynebacterium glutamicum

<400> 860

Met Ser Val Val Gly Thr Gly Leu Phe Phe Gly Ser Pro Glu Glu Glu
 1 5 10 15

Arg Asp Lys Leu Met Gln Ser Leu Met Asp Gln Lys Asn Lys Leu Ser
 20 25 30

Lys Ser Glu Gly Ile Pro Leu Val Thr Leu Asn Asp Gly Lys Thr Ile
 35 40 45

Pro Gln Leu Gly Phe Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu
 50 55 60

Arg Val Val Thr Glu Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr
 65 70 75 80

Ala Ala Ile Tyr Gly Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys
 85 90 95

Ser Gly Ile Pro Arg Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn
 100 105 110

Asp Arg His Leu Asp Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys
 115 120 125

Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Val His Trp Pro Ala Pro
 130 135 140

Lys Asn Asp Asn Tyr Val Ala Ala Trp Lys Gly Leu Glu Lys Leu Gly
 145 150 155 160
 Asp Arg Ala Arg Ser Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu
 165 170 175
 Glu Lys Leu Leu Ala Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile
 180 185 190
 Glu Leu His Pro Ala Leu Gln Gln Arg Asp Ala Val Glu Ala Ser Leu
 195 200 205
 Ala Ala Gly Ile Thr Val Glu Ser Trp Gly Pro Leu Gly Gln Gly Arg
 210 215 220
 Phe Asp Leu Gly Ala Glu Glu Pro Ile Ala Ala Ala Lys Asn His
 225 230 235 240
 Gly Lys Thr Pro Ala Gln Val Val Ile Arg Trp His Leu Gln Asn Gly
 245 250 255
 Phe Val Val Phe Pro Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn
 260 265 270
 Ile Asp Val Phe Asp Phe Glu Leu Ser Asp Glu Glu Met Ala Ala Ile
 275 280 285
 Thr Ala Leu Glu Arg Asn Asp Arg Gly Gly Ser His Pro Asn Asp Leu
 290 295 300
 Asn
 305

<210> 861
 <211> 1683
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)...(1660)
 <223> RXS00389

<400> 861
 ccaccactgc gtaacctttc cgagcaagat atcgcggaacc tgtcggattt gcttgccacc 60
 tctggcgcag gttcctaccg ccttcagttg aggtgaaagc atg atc acc gca acc 115
 Met Ile Thr Ala Thr
 1 5
 gca ctg cat ggg tgt tca ctg att gat ggc gag tgg gtc gct gga aaa 163
 Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu Trp Val Ala Gly Lys
 10 15 20
 aat ggt gag att aca gga ttc gat ccg cgc acc aat gcg agt ctg aac 211
 Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr Asn Ala Ser Leu Asn
 25 30 35
 cct tcc tac tct tta gca aac agc gca cag ctg cgc gcc gcc aca aca 259

Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu Arg Ala Ala Thr Thr
40 45 50

tgc gcg aag cga gct ttt gaa agc tac cga ctc act act cca gag gtt 307
Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu Thr Thr Pro Glu Val
55 60 65

aga gca gat ttc ctg gat tcc atc gct gac aac atc gat gcg cta tcc 355
Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn Ile Asp Ala Leu Ser
70 75 80 85

ggc gag atc gtg caa cgg gcg agc ctg gag aca ggt ttg gga act acc 403
Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr Gly Leu Gly Thr Thr
90 95 100

cga ctc aca ggc gaa gta gcc cgc acc agc aac cag ctc cgc ctg ttt 451
Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn Gln Leu Arg Leu Phe
105 110 115

gca gaa acc gtg aga agc gga cag ttc cac cga gta cgc att gaa cga 499
Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg Val Arg Ile Glu Arg
120 125 130

gga ccg cgg att gat ctt cgc cag cgt cag gtt ccg ttg gga cca gtc 547
Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val Pro Leu Gly Pro Val
135 140 145

gcg gta ttc ggg gca agc aac ttc ccc gtc gct ttc tct act gct ggt 595
Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala Phe Ser Thr Ala Gly
150 155 160 165

ggc gat aca gca tca gcg ttg gct gca ggc tgc cct gtg gtt ttt aag 643
Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys Pro Val Val Phe Lys
170 175 180

gcg cat aat gcg cac cct gga aca gct gag ctc gtc ggg caa gcg gtg 691
Ala His Asn Ala His Pro Gly Thr Ala Glu Leu Val Gly Gln Ala Val
185 190 195

cgg gga gcc gtc gaa aag cat gag ttt gat gct ggt gtg ttt aac ctt 739
Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala Gly Val Phe Asn Leu
200 205 210

gtc tac ggc cgt ggc gtg gaa att ggc cag gag ctg gct gcg gat ccg 787
Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu Leu Ala Ala Asp Pro
215 220 225

aat atc acg gca atc ggt ttt acc ggt tca cgc cag ggt ggt ttg gca 835
Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg Gln Gly Gly Leu Ala
230 235 240 245

ctg tca cag act gcg ttt agc cgc cca gtt ccc gtt cca gtc ttt gca 883
Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro Val Pro Val Phe Ala
250 255 260

gaa atg agt gcc acc aac cct gtg ttc gtc ttc ccc ggc gcg ctg gcg 931
Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe Pro Gly Ala Leu Ala
265 270 275

gat ttg gat gca tgc agt tcc ttg gct gag gcg ttt acc gct tcc gtc 979
Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala Phe Thr Ala Ser Val

280	285	290
acc ggc agt tcc ggg caa ttg tgc acc aag cct ggc ctc gtt ttc atc 1027		
Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro Gly Leu Val Phe Ile 295 300 305		
ccg cgc ggt gtt gtt ggt gat gct ttt gtg gcg ctc gta gca gcc aaa 1075		
Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala Leu Val Ala Ala Lys 310 315 320 325		
ttt aaa gaa acc acg ggt caa acg atg ctc acg caa ggc atc gct cag 1123		
Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr Gln Gly Ile Ala Gln 330 335 340		
gca tgg cag cgc gga gtc gac aac ctt gca gca cag cca agt gta aaa 1171		
Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala Gln Pro Ser Val Lys 345 350 355		
atc ctc gcc caa ggc acc ccc gga gat gga gag aac gcg ccg ggc ccg 1219		
Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu Asn Ala Pro Gly Pro 360 365 370		
gtg gtg ttt gaa agt gat gtg cag gcg ttg cta aat aat gtg gtg ttg 1267		
Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu Asn Asn Val Val Leu 375 380 385		
cag gaa gaa atc ttc ggt gcg gca tcg ctg gtg gtg cgt tat gat tcc 1315		
Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val Val Arg Tyr Asp Ser 390 395 400 405		
ccg gat caa ctc cac caa gta gcc aat tca ctc gag gga caa tta aca 1363		
Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu Glu Gly Gln Leu Thr 410 415 420		
gcc acg atc cac gca tcc cag gat gat ttc cag gaa gtc tcc aaa ctt 1411		
Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln Glu Val Ser Lys Leu 425 430 435		
atc ccc ctc ttg gag gat ctc gcg ggc cgt gtt ctt tac ggc ggc tgg 1459		
Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val Leu Tyr Gly Gly Trp 440 445 450		
cca acg ggt gtg gaa gtt ggg cac acg gtt atc cat gga ggc cct tat 1507		
Pro Thr Gly Val Glu Val Gly His Thr Val Ile His Gly Gly Pro Tyr 455 460 465		
ccg gcg acc tca aat gcg cag tcg aca agt gtt gga acc ctg gca atc 1555		
Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile 470 475 480 485		

gag aga ttt atg cgc ccg gtt tct tat caa act ttc ccg gct gag ctg
1603

Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr Phe Pro Ala Glu Leu
490 495 500

ctt cca gat cca gtt tct gag gcg aat aaa tgg gct gta cct cgg gaa
1651

Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp Ala Val Pro Arg Glu
505 510 515

ata gac cgt taatagctgg tctttacatt tgc
1683

Ile Asp Arg
520

<210> 862

<211> 520

<212> PRT

<213> Corynebacterium glutamicum

<400> 862

Met Ile Thr Ala Thr Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu
1 5 10 15

Trp Val Ala Gly Lys Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr
20 25 30

Asn Ala Ser Leu Asn Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu
35 40 45

Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu
50 55 60

Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn
65 70 75 80

Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr
85 90 95

Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn
100 105 110

Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg
115 120 125

Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val
130 135 140

Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala
145 150 155 160

Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys
165 170 175

Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu
180 185 190

Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala
195 200 205

Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu
 210 215 220
 Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg
 225 230 235 240
 Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro
 245 250 255
 Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe
 260 265 270
 Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala
 275 280 285
 Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro
 290 295 300
 Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala
 305 310 315 320
 Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr
 325 330 335
 Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala
 340 345 350
 Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu
 355 360 365
 Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu
 370 375 380
 Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val
 385 390 395 400
 Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu
 405 410 415
 Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln
 420 425 430
 Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val
 435 440 445
 Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile
 450 455 460
 His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val
 465 470 475 480
 Gly Thr Leu Ala Ile Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr
 485 490 495
 Phe Pro Ala Glu Leu Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp
 500 505 510
 Ala Val Pro Arg Glu Ile Asp Arg
 515 520

```
<220>  
<221> CDS  
<222> (101)..(859)  
<223> RXS00419
```

[illegible]

gcc aac gta ttg gtg gtt cgc cca ggc cag gta cgc acc aag atg tcc 691
 Ala Asn Val Leu Val Val Arg Pro Gly Gln Val Arg Thr Lys Met Ser
 185 190 195

gca gat ggt ggc gaa gcc cca ctg acc gtc aac cgc gaa gac gtg gca 739
 Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn Arg Glu Asp Val Ala
 200 205 210

gat gct gtt tat gat gca gtg gtg aac aag aag gac atc atc ttt gtc 787
 Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys Asp Ile Ile Phe Val
 215 220 225

cac cca ctg ttc cag tac gtc tct ttt gcg ttc caa ttc att ccg cga 835
 His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe Gln Phe Ile Pro Arg
 230 235 240 245

gca atc ttc cgc aag ctg ccg ttc taacggaagt tacggaagtt acg 882
 Ala Ile Phe Arg Lys Leu Pro Phe
 250

<210> 864

<211> 253

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 864

Met Leu Asn Ala Val Gly Lys Ala Gln Asn Ile Leu Leu Leu Gly Gly
 1 5 10 15

Thr Ser Glu Ile Gly Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly
 20 25 30

Pro Ser His Val Thr Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp
 35 40 45

Ala Ala Val Ala Glu Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val
 50 55 60

Val Asp Phe Asp Ala Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp
 65 70 75 80

Ala Ala Phe Glu Asn Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly
 85 90 95

Ile Leu Gly Asp Asn Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val
 100 105 110

Glu Ala Thr Thr Val Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu
 115 120 125

Leu Gly Gln Lys Phe Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu
 130 135 140

Ser Ser Val Ala Gly Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly
 145 150 155 160

Ser Ala Lys Ala Gly Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala
 165 170 175

Leu Arg Gly Ser Gly Ala Asn Val Leu Val Val Arg Pro Gly Gln Val
 180 185 190

Arg Thr Lys Met Ser Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn
 195 200 205

Arg Glu Asp Val Ala Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys
 210 215 220

Asp Ile Ile Phe Val His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe
 225 230 235 240

Gln Phe Ile Pro Arg Ala Ile Phe Arg Lys Leu Pro Phe
 245 250

<210> 865

<211> 1673

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1650)

<223> RXC00416

<400> 865

ctg gcg tct tac tta agc cca act gcg ctg gtg gtt gcg gtg ttg gct 48
 Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
 1 5 10 15

att ccg ctg tct gcg acc cgc ctg tat ttg gac gga atc agc gtt gac 96
 Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
 20 25 30

cag ggc ttt aga act cag ttt tta acc cgc atg gct gac gat atc ggc 144
 Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
 35 40 45

ttg tcg gac atg aac tac atc gat atg cct acc ttc tac cct gct gga 192
 Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
 50 55 60

tgg ttc tgg ctc ggt ggt cgc ttg gcc aat ctt ttg ggg ctg ccc ggt 240
 Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65 70 75 80

tgg gaa gct ttc cag cca tgg gca att gtg tcc atg gca gtt gct gct 288
 Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
 85 90 95

tct gtg tta gtt cca gtg tgg cag cgc atc acc ggt tcc ctg ccg gtg 336
 Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
 100 105 110

gca aca ggc att gcg ttg gtg aca acc tgc att atc ttg gcg atg aat 384
 Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
 115 120 125

tcc gaa gag ccc tac gct gca atc gtt gcg atg ggt att cca gcg atg 432
 Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met

130	135	140	
ctc gtg ctg gct tcc cgc att gcc aag ggc gat aag ttt gcg ctt gcc			480
Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala			
145	150	155	160
ggc ggc att att tac ttg ggt gtt tcg gct act ttc tat act ttg ttc			528
Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe			
	165	170	175
acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg			576
Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala			
	180	185	190
gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg			624
Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu			
	195	200	205
ggg ggt gga tcc att gtc att gcg ttg att tct tgg ggt cct tac ctt			672
Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu			
	210	215	220
ctg gcc tcc atc aac gga gcg gag cgc tct ggc gat tcc gca aca cac			720
Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His			
	225	230	240
tac ctg cct ctt gaa ggc acc caa ttc ccg gtt cct ttc ttg gca tca			768
Tyr Leu Pro Leu Gln Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser			
	245	250	255
agc gtt gtg gga ctg ttg tgt ctt gtt ggc ctg atc tat ttg gtg gtg			816
Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val			
	260	265	270
cgt ttc cac aac aat gag gtg cgc gcg atg tgg gtc ggc atc gca gtg			864
Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val			
	275	280	285
ttt tat gcc tgg atg ggc atg tcc atg gcg atc acg ctt ttg ggc aac			912
Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn			
	290	295	300
acg ttg ctt gga ttc cgt ctt gat acg gtg ctg gtg ctt att ttt gcc			860
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala			
305	310	315	320
acg gct gga gtg ttg ggc att gca gat ttc cgc ctt gcc agt gtg tat			1008
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr			
	325	330	335
cag ctc tac ccc acc caa atc aca gag cgc acg gcc acc cat ctg acc			1056
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr			
	340	345	350
aat cta att gtg gtc ctc gtg ctg ctt ggc ggc ctc tac tac gcg caa			1104
Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln			
	355	360	365

gat ctg ccg cag aag aac gca cga gct atc gat ctg gcc tat acc gat
1152

Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp
370 375 380

act gat ggc tac ggc gag cgc gcg gat ctg tat ccg gcc gga gct gca
1200

Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala
385 390 395 400

cgt tat tac aag gac atc aac gat cat ctg ctt gat caa gga ttc gag
1248

Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu
405 410 415

cct tcc gaa act gtc gtg ctg aca gac gaa ctc gat ttc atg tcc tac
1296

Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr
420 425 430

tac cct tat cgc gga tac caa gct ttt act tcc cac tac gcc aac ccg
1344

Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro
435 440 445

ctt ggt gag ttc gga aac agg aac gca ttc atc gaa gat ctc gcg atc
1392

Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile
450 455 460

cga agc tgg gat gag ttg gct gat cct caa caa ttc agc gac gcc ttg
1440

Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu
465 470 475 480

aac acc tct cca tgg acg atc cct gag gtg ttc atc ttc cgt ggc tcc
1488

Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser
485 490 495

atc gat gat cct gac gcc ggt tgg aaa tac gac gtg gct gaa gat ctg
1536

Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu
500 505 510

tac ccg aac aat cca aac gtg cgc ttc cgc ggc gtg tac ttt aac ccg
1584

Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro
515 520 525

gag tca ttt gat cag atg tgg cag acc aag caa gtg gga cct ttc gtg
1632

Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val
530 535 540

gtg gta acg cac aat gag taattcctca ccaaacgacc caa
1673

Val Val Thr His Asn Glu
545 550

<210> 866

<211> 550

<212> PRT

<213> Corynebacterium glutamicum

<400> 866

Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
 1 5 10 15

Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
 20 25 30

Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
 35 40 45

Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
 50 55 60

Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65 70 75 80

Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
 85 90 95

Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
 100 105 110

Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
 115 120 125

Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
 130 135 140

Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
 145 150 155 160

Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
 165 170 175

Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
 180 185 190

Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
 195 200 205

Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
 210 215 220

Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
 225 230 235 240

Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
 245 250 255

Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
 260 265 270

Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
 275 280 285

Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn

290	295	300
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala 305 310 315 320		
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr 325 330 335		
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr 340 345 350		
Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln 355 360 365		
Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp 370 375 380		
Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala 385 390 395 400		
Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu 405 410 415		
Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr 420 425 430		
Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro 435 440 445		
Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile 450 455 460		
Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu 465 470 475 480		
Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser 485 490 495		
Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu 500 505 510		
Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro 515 520 525		
Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val 530 535 540		
Val Val Thr His Asn Glu 545 550		

<210> 867
 <211> 1059
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1036)
 <223> RXC02206

<400> 867

```

ggcaggatct gctgctgcgg ctaggagggt tatctcttca ttcacccgat ctaccgtact 60
accttatgac ctacagtagtg tgggtgggcgt gaaacagcga atg gtc ggt tca agt 115
                                         Met Val Gly Ser Ser
                                         1           5

ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser
                        10           15           20

ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn
                        25           30           35

tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc 259
Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val
                        40           45           50

gcg gaa gaa atg ctc ggc acg gttg ttg gat gcg gaa gtc tct cgt tcg 307
Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser
                        55           60           65

gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc 355
Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu
                        70           75           80           85

ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat 403
Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp
                        90           95           100

gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg 451
Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val
                        105           110           115

ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg 499
Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu
                        120           125           130

gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga 547
Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly
                        135           140           145

tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca 595
Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala
                        150           155           160           165

gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg 643
Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu
                        170           175           180

ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta 691
Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu
                        185           190           195

ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act 739
Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr
                        200           205           210

gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca 787
Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr

```

215 220 225
 gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc 835
 Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile
 230 235 240 245
 att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc 883
 Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro
 250 255 260
 gct gtc aca gcc acc acc tgg gtg cgt gat cgt ccc gga gtg aca gct 931
 Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala
 265 270 275
 gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag 979
 Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys
 280 285 290
 gcg gaa tcg gtg act ttg cca aca cca atc caa gcc ctt gat gat
 1027
 Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp
 295 300 305
 gtc tcc ctg tgacttggtc caattacatt cac
 1059
 Val Ser Leu
 310

 <210> 868
 <211> 312
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 868
 Met Val Gly Ser Ser Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr
 1 5 10 15
 Ser Thr Trp Gly Ser Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe
 20 25 30
 Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn
 35 40 45
 Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala
 50 55 60
 Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn
 65 70 75 80
 Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu
 85 90 95
 Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu
 100 105 110
 Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu
 115 120 125
 Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr
 130 135 140

Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala
145 150 155 160

Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln
165 170 175

Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro
180 185 190

Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly
195 200 205

Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser
210 215 220

Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
225 230 235 240

Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
245 250 255

Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg
260 265 270

Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu
275 280 285

Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr
290 295 300

Gln Ala Leu Asp Asp Val Ser Leu
305 310

<210> 869

<211> 621

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (598)

<223> RXS03074

<400> 869

tttgtgggca atctggtttt ttcgtaattg tgtgggatga atctctttaa aattcacatt 60

tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115
Met Thr Gln Ser Ala
1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259

Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165
 cag taatttggtt tgacgacgca gta 621
 Gln

<210> 870

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 870

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
 1 5 10 15
 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
 20 25 30
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr

100	105	110
Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr		
115	120	125
Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe		
130	135	140
Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr		
145	150	155
160		
Glu Ala Pro Ile Lys Gln		
165		

<210> 871

<211> 621

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(598)

<223> FRXA02906

<400> 871

```

tttgtgggca atctggtttt ttcgtaattg tgtgggatga atctcttaaa aattcacatt 60
tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115
                                Met Thr Gln Ser Ala
                                1                               5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
                                10                               15                               20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
                                25                               30                               35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
                                40                               45                               50

```

```

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
                                55                               60                               65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
                                70                               75                               80                               85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
                                90                               95                               100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
                                105                               110                               115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499

```

Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130

gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165

cag taatttggtt tgacgacga gta 621
 Gln

<210> 872

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 872

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
 1 5 10 15

Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
 20 25 30

Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160

Glu Ala Pro Ile Lys Gln
 165

<210> 873

<211> 1752

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1729)

<223> RXA02315

<400> 873

```

cgtttgga cgttgctgc cagcaaagat aggcgtgatt ggtggtttga gcgcgtgcgt 60

gaatcgatc cgtacctgga gacgatctag actgttgctgc atg tcc agc acg cca 115
                                         Met Ser Ser Thr Pro
                                         1           5

gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163
Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val
                        10                        15                        20

act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tcg ctt 211
Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu
                        25                        30                        35

gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag 259
Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu
                        40                        45                        50

cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg 307
Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg
                        55                        60                        65

ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg 355
Pro Val Ala Val Val Met Thr Ser Gly Thr Ala Val Ala Asn Cys Leu
                        70                        75                        80                        85

cct gct gtt gct gaa gct gcg cat gcc cat atc ccg ttg att gtg ctc 403
Pro Ala Val Ala Glu Ala Ala His Ala His Ile Pro Leu Ile Val Leu
                        90                        95                        100

tct gct gac cgt cct gca cat ttg gtg gga acg ggg gcg agc caa acg 451
Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr Gly Ala Ser Gln Thr
                        105                        110                        115

att aac cag acc ggt att ttt ggt gat ctt gca ccg acg gtc ggt atc 499
Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala Pro Thr Val Gly Ile
                        120                        125                        130

act gag ctg gat cag gta gcg cag att gct gaa agc ctt gct cag ggg 547
Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu Ser Leu Ala Gln Gly
                        135                        140                        145

gct tcc cag att ccg cgt cat ttc aat ctt gca ctt gat gtt cct ttg 595
Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala Leu Asp Val Pro Leu
                        150                        155                        160                        165

gtt gct cct gaa ctg cca gag ctt cat ggt gag gca gtt gga gca tca 643
Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu Ala Val Gly Ala Ser
                        170                        175                        180

tgg acg cat cgc tgg atc aac cac ggt gag gtg acc gtg gac ctg ggg 691
Trp Thr His Arg Trp Ile Asn His Gly Glu Val Thr Val Asp Leu Gly
                        185                        190                        195

gag cac acc ctc gtg att gcc ggt gat gaa gca tgg gaa gtg gaa ggg 739

```

Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala Trp Glu Val Glu Gly
 200 205 210

ctg gaa gat gtg ccc acc atc gct gaa cct act gca cca aag cct tat 787
 Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr Ala Pro Lys Pro Tyr
 215 220 225

aat ccg gtg cac cca ctg gct gct gaa atc ttg ctg aag gag cag gtc 835
 Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu Leu Lys Glu Gln Val
 230 235 240 245

tcc gcg gaa ggc tat gtg gta aac acc agg cct gat cat gtg atc gtg 883
 Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro Asp His Val Ile Val
 250 255 260

gtg gga cac ccc acg ctg cac cgc gga gtg ttg aag ttg atg tca gat 931
 Val Gly His Pro Thr Leu His Arg Gly Val Leu Lys Leu Met Ser Asp
 265 270 275

cct ggc att aaa tta act gtg ctt tca cgc acc gat atc atc act gat 979
 Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr Asp Ile Ile Thr Asp
 280 285 290

ccc ggc cgc cat gcc gat cag gtg ggc agc aca gtg aaa gtc acc ggc
 1027
 Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr Val Lys Val Thr Gly
 295 300 305

acc cag gaa aag cag tgg cta aag atc tgt tcg gca gca tca gaa ctt
 1075
 Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser Ala Ala Ser Glu Leu
 310 315 320 325

gcg gcc gat ggt gtg cgt gac gtc ctg gac aac caa gaa ttc ggt ttc
 1123
 Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn Gln Glu Phe Gly Phe
 330 335 340

acc ggc ctc cat gtt gcc gca gcc gtg gcg gat acc tta ggc acc ggc
 1171
 Thr Gly Leu His Val Ala Ala Ala Val Ala Asp Thr Leu Gly Thr Gly
 345 350 355

gat act ctc ttt gct gca gca tcc aac tca atc cgt gac ctc tcc ctg
 1219
 Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu
 360 365 370

gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc
 1267
 Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val
 375 380 385

gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct
 1315
 Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala
 390 395 400 405

gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc
 1363
 Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala

410 415 420
 ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc
 1411
 Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile
 425 430 435
 ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac
 1459
 Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn
 440 445 450
 gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt
 1507
 Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly
 455 460 465
 ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc
 1555
 Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser
 470 475 480 485
 atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac
 1603
 Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp
 490 495 500
 aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc
 1651
 Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser
 505 510 515
 gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca
 1699
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala
 520 525 530
 caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt
 1749
 Gln Gln Gln Ala Leu Met Asp Thr Val His
 535 540

gcg
1752

<210> 874
 <211> 543
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 874
 Met Ser Ser Thr Pro Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser
 1 5 10 15
 Leu Ala Pro His Val Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn
 20 25 30
 Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His
 35 40 45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
 50 55 60
 Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
 65 70 75 80
 Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile
 85 90 95
 Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
 100 105 110
 Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
 115 120 125
 Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
 130 135 140
 Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
 145 150 155 160
 Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
 165 170 175
 Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
 180 185 190
 Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
 195 200 205
 Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
 210 215 220
 Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
 225 230 235 240
 Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
 245 250 255
 Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
 260 265 270
 Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
 275 280 285
 Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr
 0 295 300
 Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser
 305 310 315 320
 Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn
 325 330 335
 Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp
 340 345 350
 Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile
 355 360 365
 Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe

370	375	380
Ser Pro Arg Gly Val	Ala Gly Ile Asp Gly	Ser Val Ala Gln Ala Ile
385	390	395 400
Gly Thr Ser Leu Ala	Val Gln Ser Arg His	Pro Asp Glu Ile Arg Ala
405	410	415
Pro Arg Thr Val Ala	Leu Leu Gly Asp Leu	Ser Phe Leu His Asp Ile
420	425	430
Gly Gly Leu Leu Ile	Gly Pro Asp Glu Pro	Arg Pro Glu Asn Leu Thr
435	440	445
Ile Val Val Ser Asn	Asp Asn Gly Gly Gly	Ile Phe Glu Leu Leu Glu
450	455	460
Thr Gly Ala Asp Gly	Leu Arg Pro Asn Phe	Glu Arg Ala Phe Gly Thr
465	470	475 480
Pro His Asp Ala Ser	Ile Ala Asp Leu Cys	Ala Gly Tyr Gly Ile Glu
485	490	495
His Gln Val Val Asp	Asn Leu Gln Asp Leu	Ile Ile Ala Leu Val Asp
500	505	510
Thr Thr Glu Val Ser	Gly Phe Thr Ile Ile	Glu Ala Ser Thr Val Arg
515	520	525
Asp Thr Arg Arg Ala	Gln Gln Gln Ala Leu	Met Asp Thr Val His
530	535	540

<210> 875

<211> 1080

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1057)

<223> RXA02319

<400> 875

```

atgtgggtga gataaccgac cgtgatgtcg ccctagcaaa agtcacgcac gccacgccca 60
agaccttggc catttcggca gaggccttaag gttaaagatt atg agc aac tac agc 115
Met Ser Asn Tyr Ser
1 5
acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163
Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe
10 15 20
gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211
Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg
25 30 35
gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259
Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn
40 45 50

```

gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac 307
 Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His
 55 60 65

gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc 355
 Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly
 70 75 80 85

ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa 403
 Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln
 90 95 100

cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc 451
 Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg
 105 110 115

gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa 499
 Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys
 120 125 130

gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc 547
 Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg
 135 140 145

acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc 595
 Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly
 150 155 160 165

ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc 643
 Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg
 170 175 180

caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac 691
 Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp
 185 190 195

gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac 739
 Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn
 200 205 210

gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg 787
 Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met
 215 220 225

caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa 835
 Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu
 230 235 240 245

aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc 883
 Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr
 250 255 260

ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc 931
 Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu
 265 270 275

atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg 979
 Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met
 280 285 290

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa
1027

Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu
295 300 305

ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atgggggtcct
1077

Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr
310 315

aaa
1080

<210> 876

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 876

Met Ser Asn Tyr Ser Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala
1 5 10 15

Thr Val Pro Gly Phe Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His
20 25 30

Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg
35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr
50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu
65 70 75 80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys
85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala
100 105 110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp
115 120 125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val
130 135 140

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn
145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu
165 170 175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp
180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met
195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr
210 215 220

Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp
225 230 235 240

His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn
245 250 255

Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu
260 265 270

Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr
275 280 285

Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe
290 295 300

Leu Glu Lys Arg Glu Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr
305 310 315

<210> 877

<211> 1017

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(994)

<223> RXS00393

<400> 877

tctattcatt tcacaatagc gtttcacact ccccatagc ctgccgaacg tatttcaagc 60

aattgcgcga tcgagtatgt gatggggaaa gatagaggtt atg tct cac acg gaa 115
Met Ser His Thr Glu
1 5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
10 15 20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
25 30 35

gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
40 45 50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
55 60 65

tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
70 75 80 85

cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
90 95 100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
 Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
 105 110 115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
 Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
 120 125 130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
 Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
 135 140 145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
 Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
 150 155 160 165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
 170 175 180

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
 185 190 195

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
 200 205 210

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
 215 220 225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
 230 235 240 245

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
 250 255 260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc 931
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile
 265 270 275

ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg 979
 Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu
 280 285 290

gca tta gcg ttt agc taaaacgctt ttcgacgctc ccc
 1017
 Ala Leu Ala Phe Ser
 295

<210> 878

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 878

Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp

1	5	10	15
Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val	20	25	30
Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp	35	40	45
Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val	50	55	60
Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp	65	70	75
Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys	85	90	95
Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala	100	105	110
Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly	115	120	125
Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro	130	135	140
Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly	145	150	155
Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser	165	170	175
Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly	180	185	190
Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr	195	200	205
Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys	210	215	220
Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu	225	230	235
Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu	245	250	255
Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp	260	265	270
Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala	275	280	285
Val Leu Thr Gly Leu Ala Leu Ala Phe Ser	290	295	

<210> 879

<211> 1005

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(982)

<223> FRXA00393

<400> 879

```

tctattcatt tcacaatagc gtttcacact ccccatagc ctgccgaacg tatttcaagc 60

aattgcgcga tcgagtatgt gatggggaaa gatagagggtt atg tct cac acg gaa 115
                                         Met Ser His Thr Glu
                                         1                               5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
                        10                               15                               20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
                        25                               30                               35

gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
                        40                               45                               50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
                        55                               60                               65

tac tct gat ggc att ctc ggc acc gat gaa gac cgc acc ggt cct ctg 355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
                        70                               75                               80                               85

cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
                        90                               95                               100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
                        105                               110                               115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
                        120                               125                               130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
                        135                               140                               145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
                        150                               155                               160                               165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
                        170                               175                               180

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
                        185                               190                               195

```

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
 200 205 210

 gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
 215 220 225

 att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
 230 235 240 245

 cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
 250 255 260

 ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tgc 931
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser
 265 270 275

 gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979
 Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro Cys Ser Arg Ala Trp
 280 285 290

 cat tagcgttttag ctaaaacgct ttt
 1005
 His

<210> 880
 <211> 294
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 880
 Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp
 1 5 10 15

 Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val
 20 25 30

 Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
 35 40 45

 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
 50 55 60

 Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
 65 70 75 80

 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
 85 90 95

 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
 100 105 110

 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
 115 120 125

 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro


```
<210> 881
<211> 843
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(820)
<223> RXA00391
```

<400> 881																	
atcttgtaga tcccaccgca attctgggag atctcgagga cgcaatctct ggaagaaaac																60	
tttctctccc atccctgtac aagataaaac ccgtgcacag ttg ctg cgc gat tct																115	
											Leu	Leu	Arg	Asp	Ser		
											1				5		
caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc																163	
Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala																	
											10				15		20
act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg																211	
Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu																	
											25				30		35
aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa																259	
Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu																	
											40				45		50

ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag 307
 Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln
 55 60 65

gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat 355
 Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp
 70 75 80 85

ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa 403
 Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu
 90 95 100

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln
 105 110 115

tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu
 120 125 130

ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg
 135 140 145

att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser
 150 155 160 165

tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc gcc 643
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly
 170 175 180

gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met
 185 190 195

att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn
 200 205 210

gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile
 215 220 225

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His
 230 235 240

tgc 843

<210> 882

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 882

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile
 1 5 10 15

```
<210> 883
<211> 384
<212> DNA
<213> Corynebacterium glutamicum
```

```
<400> 883
gccaacgagg gttggtttac cacctctgat tcaggtgaac tccacgacgg gattctcacc 60
gtgactggtc gcgtaggatac ccgtcattga ttccgggtgga ttg aag ttg cac cca 115
Leu Lys Leu His Pro
```

	1	5	
gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg			163
Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala			
	10	15	20
tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc			211
Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala			
	25	30	35
gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac			259
Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp			
	40	45	50
gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct			307
Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser			
	55	60	65
ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag			355
Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys			
	70	75	80
ctg ttt tagtcttcat tcttgctggc tgc			384
Leu Phe			

<210> 884

<211> 87

<212> PRT

<213> Corynebacterium glutamicum

<400> 884

Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys
 1 5 10 15

Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly
 20 25 30

Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val
 35 40 45

Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu
 50 55 60

Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg
 65 70 75 80

Arg Ala Ile Ala Lys Leu Phe
 85

<210> 885

<211> 705

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(682)

<223> RXA00997

<400> 885

```

cccatctgtg gcagatcgaa tgcaccacc gcggagaagt cgtcgcacga accacactgc 60
gcaccatggg gctgaacaag tagccctata ctcgggcacc atg act aca tgg aaa 115
                                     Met Thr Thr Trp Lys
                                     1 5
gag ctc aca gat aac aac cca gcg cac tca gaa aac tac gcg cag cgc 163
Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu Asn Tyr Ala Gln Arg
                                     10 15 20
tgg cga aac ctc gcc gca gca ggc aat gat att tac ggc gaa gcc cgc 211
Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile Tyr Gly Glu Ala Arg
                                     25 30 35
ctc att gat gcc atg gca ccc agg gga gcg aaa atc ttg gat gct ggc 259
Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys Ile Leu Asp Ala Gly
                                     40 45 50
tgc ggc cag gga cgc atc ggt ggc tac ctg tcc aag caa ggc cac gat 307
Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser Lys Gln Gly His Asp
                                     55 60 65
gtt cta ggc aca gac ctt gat ccc atc ctg att gat tac gcc aag cag 355
Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile Asp Tyr Ala Lys Gln
                                     70 75 80 85
gac ttt cca gaa gct cgc tgg gtg gtg gga gat ctc tct gtt gat cag 403
Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp Leu Ser Val Asp Gln
                                     90 95 100
atc tca gag act gat ttt gat ctc att gtc tcc gcc ggc aac gtc atg 451
Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser Ala Gly Asn Val Met
                                     105 110 115
ggc ttt ctc gct gag gat ggt cgc gaa cct gca cta gcc aac att cac 499
Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala Leu Ala Asn Ile His
                                     120 125 130
cgc gca ctg ggc gcc gat ggc cgc gct gtc atc ggt ttc ggc gca gga 547
Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile Gly Phe Gly Ala Gly
                                     135 140 145
cgt gga tgg gtc ttt gga gac ttc ctc gaa gtc gca gaa cgc gtg ggc 595
Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val Ala Glu Arg Val Gly
150 155 160 165
ctc gag ttg gaa aat gct ttt gag tct tgg gat ctt aag cct ttt gtc 643
Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp Leu Lys Pro Phe Val
170 175 180
caa ggc tct gag ttc tta gtg gcg gta ttt acc aag aag taacacctct 692
Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr Lys Lys
185 190
atcttgccacc tga 705

```

<210> 886

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 886

Met Thr Thr Trp Lys Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu
 1 5 10 15

Asn Tyr Ala Gln Arg Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile
 20 25 30

Tyr Gly Glu Ala Arg Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys
 35 40 45

Ile Leu Asp Ala Gly Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser
 50 55 60

Lys Gln Gly His Asp Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile
 65 70 75 80

Asp Tyr Ala Lys Gln Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp
 85 90 95

Leu Ser Val Asp Gln Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser
 100 105 110

Ala Gly Asn Val Met Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala
 115 120 125

Leu Ala Asn Ile His Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile
 130 135 140

Gly Phe Gly Ala Gly Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val
 145 150 155 160

Ala Glu Arg Val Gly Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp
 165 170 175

Leu Lys Pro Phe Val Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr
 180 185 190

Lys Lys

<210> 887

<211> 861

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(838)

<223> RXA02189

<400> 887

aatggcaaaa atgggcacat acgatactga tgggaccaat gggaaaacct caagccacca 60

attgagccag ttctctcaag caaacggata ctggtgggat gtg gac gcg gcc gac 115
 Val Asp Ala Ala Asp
 1 5

tat cac gaa cgc cac cct tct tat tta ggc acg gat tcc gct cac ggc	163
Tyr His Glu Arg His Pro Ser Tyr Leu Gly Thr Asp Ser Ala His Gly	
10 15 20	
gag ttc tac tgg tgc ccc gag atg ctg cat gaa aaa gat gta cgt ctt	211
Glu Phe Tyr Trp Cys Pro Glu Met Leu His Glu Lys Asp Val Arg Leu	
25 30 35	
ctt ggc act ccc gca gca ctc tcc ggc aag aaa att tta gag atc ggt	259
Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys Ile Leu Glu Ile Gly	
40 45 50	
tgc ggc tcg gca ccg tgt gct cgg tgg ctg gcc aat gat gtt ccg aat	307
Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala Asn Asp Val Pro Asn	
55 60 65	
gcc ttt gtc acc gct ttc gac att tct tca caa atg ctc aaa tac gca	355
Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln Met Leu Lys Tyr Ala	
70 75 80 85	
ggg cac gac cat aac gta cac ctc gta cag gcc gat gca atg tca ctc	403
Gly His Asp His Asn Val His Leu Val Gln Ala Asp Ala Met Ser Leu	
90 95 100	
ccc tac gcc gac agt tcc ttt gac gtg gtc ttt tcc gtt ttc ggc gcc	451
Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe Ser Val Phe Gly Ala	
105 110 115	
atc ccc ttt gtg gag gat tcc gcc gca ctc atg aag gaa atc gcg cgc	499
Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met Lys Glu Ile Ala Arg	
120 125 130	
gtc ctc aaa ccc ggc gga cgc ctc att ttc tcc atc acc cac ccg atg	547
Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser Ile Thr His Pro Met	
135 140 145	
cgc tgg att ttc ctc gac gat ccc ggc ccc gca ggc ctc acc gcg atc	595
Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala Gly Leu Thr Ala Ile	
150 155 160 165	
acc agc tac ttc gac cag cgc ggc tac gtc gaa gaa gac gag gaa acc	643
Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu Glu Asp Glu Glu Thr	
170 175 180	
ggg gct tta agc tat gcg gaa cag cac cgc acc atg ggc gcg ccg atc	691
Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr Met Gly Ala Arg Ile	
185 190 195	
aat gag ctt atc gac gcc tcc ctc cac tta gat cac ctc atc gaa cca	739
Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp His Leu Ile Glu Pro	
200 205 210	
gaa tgg cca gat gag ttg gaa gaa aac tgg ggc caa tgg tca cca ctt	787
Glu Trp Pro Asp Glu Leu Glu Asn Trp Gly Gln Trp Ser Pro Leu	
215 220 225	
cga gga aag ctc ttc ccc ggg aca gca atc ttc ctc gcc acg tac cgc	835
Arg Gly Lys Leu Phe Pro Gly Thr Ala Ile Phe Leu Ala Thr Tyr Arg	
230 235 240 245	
ccc taaaaaacca acggcgctca ttt	861

Pro

<210> 888

<211> 246

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 888

Val Asp Ala Ala Asp Tyr His Glu Arg His Pro Ser Tyr Leu Gly Thr
 1 5 10 15

Asp Ser Ala His Gly Glu Phe Tyr Trp Cys Pro Glu Met Leu His Glu
 20 25 30

Lys Asp Val Arg Leu Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys
 35 40 45

Ile Leu Glu Ile Gly Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala
 50 55 60

Asn Asp Val Pro Asn Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln
 65 70 75 80

Met Leu Lys Tyr Ala Gly His Asp His Asn Val His Leu Val Gln Ala
 85 90 95

Asp Ala Met Ser Leu Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe
 100 105 110

Ser Val Phe Gly Ala Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met
 115 120 125

Lys Glu Ile Ala Arg Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser
 130 135 140

Ile Thr His Pro Met Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala
 145 150 155 160

Gly Leu Thr Ala Ile Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu
 165 170 175

Glu Asp Glu Glu Thr Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr
 180 185 190

Met Gly Ala Arg Ile Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp
 195 200 205

His Leu Ile Glu Pro Glu Trp Pro Asp Glu Leu Glu Glu Asn Trp Gly
 210 215 220

Gln Trp Ser Pro Leu Arg Gly Lys Leu Phe Pro Gly Thr Ala Ile Phe
 225 230 235 240

Leu Ala Thr Tyr Arg Pro
 245

<210> 889

<211> 813

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(790)

<223> RXA02311

<400> 889

cattttgggt atcgggttgg tgtccatcgg tggagctaag ggcgctaagc atcgcagcca 60

aataacctcc	cactaaagct	cctggggttag	actcgaacgc	gtg	gct	aaa	gca	gat	115
				Val	Ala	Lys	Ala	Asp	
				1				5	

tta	gac	aag	gac	ccc	ttc	gac	gta	gcg	tca	atg	ttc	gat	gac	gtc	gga	163
Leu	Asp	Lys	Asp	Pro	Phe	Asp	Val	Ala	Ser	Met	Phe	Asp	Asp	Val	Gly	
				10				15						20		

aag	aac	tac	gat	ctc	acc	aat	acc	gtg	ctt	tct	ttt	ggg	cag	gac	cgt	211
Lys	Asn	Tyr	Asp	Leu	Thr	Asn	Thr	Val	Leu	Ser	Phe	Gly	Gln	Asp	Arg	
			25					30					35			

gtg	tgg	cga	aag	cgc	act	agg	cag	cgc	ctg	gac	ctc	aag	cca	ggg	gag	259
Val	Trp	Arg	Lys	Arg	Thr	Arg	Gln	Arg	Leu	Asp	Leu	Lys	Pro	Gly	Glu	
		40					45					50				

aag	gtg	ctt	gat	cta	gct	gca	gga	aca	gcc	gtt	tcc	acc	gtg	gag	ttg	307
Lys	Val	Leu	Asp	Leu	Ala	Ala	Gly	Thr	Ala	Val	Ser	Thr	Val	Glu	Leu	
	55					60					65					

gca	aaa	tcc	ggc	gcg	ttt	tgt	gtg	gcg	tgt	gat	ttc	tcc	cag	ggc	atg	355
Ala	Lys	Ser	Gly	Ala	Phe	Cys	Val	Ala	Cys	Asp	Phe	Ser	Gln	Gly	Met	
	70				75					80				85		

ctc	gcc	gca	ggg	aaa	gac	cgc	gat	gtg	tcc	aag	gtt	gtg	ggc	gat	ggc	403
Leu	Ala	Ala	Gly	Lys	Asp	Arg	Asp	Val	Ser	Lys	Val	Val	Gly	Asp	Gly	
				90					95					100		

atg	cag	ttg	ccg	ttt	gca	gac	aac	agc	ttt	gat	gct	gtg	acc	att	tct	451
Met	Gln	Leu	Pro	Phe	Ala	Asp	Asn	Ser	Phe	Asp	Ala	Val	Thr	Ile	Ser	
			105					110					115			

tat	ggc	ctg	cgc	aat	att	cac	gat	ttc	cgc	gct	ggc	ctg	aaa	gaa	atg	499
Tyr	Gly	Leu	Arg	Asn	Ile	His	Asp	Phe	Arg	Ala	Gly	Leu	Lys	Glu	Met	
		120					125					130				

gcc	cgc	gtg	act	aaa	cct	ggg	gga	cgc	ctc	acc	gtg	gcg	gag	ttc	tcc	547
Ala	Arg	Val	Thr	Lys	Pro	Gly	Gly	Arg	Leu	Thr	Val	Ala	Glu	Phe	Ser	
	135					140					145					

acc	ccc	gtg	atc	cct	gtg	ttc	ggc	acc	gtg	tac	aag	gag	tac	ctc	atg	595
Thr	Pro	Val	Ile	Pro	Val	Phe	Gly	Thr	Val	Tyr	Lys	Glu	Tyr	Leu	Met	
	150				155				160					165		

cgc	ctg	ctg	ccc	cag	gcg	gcg	cgc	gca	gta	tcg	tcc	aac	ccg	gag	gcc	643
Arg	Leu	Leu	Pro	Gln	Ala	Ala	Arg	Ala	Val	Ser	Ser	Asn	Pro	Glu	Ala	
			170					175						180		

tac	att	tac	ctg	gct	gat	tcc	atc	cgc	gca	tgg	cct	agc	cag	gcg	gaa	691
Tyr	Ile	Tyr	Leu	Ala	Asp	Ser	Ile	Arg	Ala	Trp	Pro	Ser	Gln	Ala	Glu	

```

185              190              195
cta gca cgg gag atc aac cag aat ggt tgg tca gat tgc ggt tgg cag 739
Leu Ala Arg Glu Ile Asn Gln Asn Gly Trp Ser Asp Cys Gly Trp Gln
      200              205              210

aac ctg acc ttc ggc atc gtc gcg ctg cac tcg gcg att aaa cca gag 787
Asn Leu Thr Phe Gly Ile Val Ala Leu His Ser Ala Ile Lys Pro Glu
      215              220              225

aac tagtcgagtc ccacagaggg gag 813
Asn
230

<210> 890
<211> 230
<212> PRT
<213> Corynebacterium glutamicum

<400> 890
Val Ala Lys Ala Asp Leu Asp Lys Asp Pro Phe Asp Val Ala Ser Met
  1              5              10              15

Phe Asp Asp Val Gly Lys Asn Tyr Asp Leu Thr Asn Thr Val Leu Ser
      20              25              30

Phe Gly Gln Asp Arg Val Trp Arg Lys Arg Thr Arg Gln Arg Leu Asp
      35              40              45

Leu Lys Pro Gly Glu Lys Val Leu Asp Leu Ala Ala Gly Thr Ala Val
      50              55              60

Ser Thr Val Glu Leu Ala Lys Ser Gly Ala Phe Cys Val Ala Cys Asp
      65              70              75              80

Phe Ser Gln Gly Met Leu Ala Ala Gly Lys Asp Arg Asp Val Ser Lys
      85              90              95

Val Val Gly Asp Gly Met Gln Leu Pro Phe Ala Asp Asn Ser Phe Asp
      100              105              110

Ala Val Thr Ile Ser Tyr Gly Leu Arg Asn Ile His Asp Phe Arg Ala
      115              120              125

Gly Leu Lys Glu Met Ala Arg Val Thr Lys Pro Gly Gly Arg Leu Thr
      130              135              140

Val Ala Glu Phe Ser Thr Pro Val Ile Pro Val Phe Gly Thr Val Tyr
      145              150              155              160

Lys Glu Tyr Leu Met Arg Leu Leu Pro Gln Ala Ala Arg Ala Val Ser
      165              170              175

Ser Asn Pro Glu Ala Tyr Ile Tyr Leu Ala Asp Ser Ile Arg Ala Trp
      180              185              190

Pro Ser Gln Ala Glu Leu Ala Arg Glu Ile Asn Gln Asn Gly Trp Ser
      195              200              205

Asp Cys Gly Trp Gln Asn Leu Thr Phe Gly Ile Val Ala Leu His Ser

```

210 215 220

Ala Ile Lys Pro Glu Asn
225 230

<210> 891
<211> 876
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(853)
<223> RXN02912

<400> 891
catcgggtgtc ggttcactga tgggtggccaa gaaggttgga taacagggtt aatcttgggt 60
gatattgaaa tgacgtattc ctgattgggc tgaaaaatct gtg aca tca cct gaa 115
Val Thr Ser Pro Glu
1 5
tta caa aac atc ctt aac aat tat tgg agc ggc agg gca gag gct tac 163
Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly Arg Ala Glu Ala Tyr
10 15 20
cac ctc aac caa acc caa agc gag cgt gca caa ttt gaa cgc ccc atc 211
His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln Phe Glu Arg Pro Ile
25 30 35
tgg gaa aag gtg tgg tcg aag gct ttg cct atc gtg tcg gaa gaa gcg 259
Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile Val Ser Glu Glu Ala
40 45 50
gta aag gtt ctc gat ctt ggc tgt ggc gct ggt tat gtc acc cac ctt 307
Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly Tyr Val Thr His Leu
55 60 65
cta agc gat tgc gga tac gaa aca atc ggc gtt gat ggt tct gag gaa 355
Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val Asp Gly Ser Glu Glu
70 75 80 85
atg atc aat caa gct acg cag gag aat ggt ctt cgc agg tcg acg ggt 403
Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu Arg Arg Ser Thr Gly
90 95 100
cgg gcg act gcc att ttt cag gtc ggg gat gcg cat gat ccc gag ttc 451
Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala His Asp Pro Glu Phe
105 110 115
cgg gaa ggc tct ttt gat gcg ata acc agc cgg tat gtg ttg tgg act 499
Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg Tyr Val Leu Trp Thr
120 125 130
ctg ctg gat ccc cag gca gcg att aat cgt tgg gtg tct ttg cta aaa 547
Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp Val Ser Leu Leu Lys
135 140 145
cct ggt ggg gtt att gcg tgc gta gat gcg gct tgg tat ccg aag ggc 595
Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala Trp Tyr Pro Lys Gly

150	155	160	165	
att gat gct ggc acg gaa gta gat tca gtg gat ggt ccg agt gct ttc				643
Ile Asp Ala Gly Thr Glu Val Asp Ser Val Asp Gly Pro Ser Ala Phe				
170		175	180	
gta gag acc tat acc ccg gaa ctt ttg agg aat ctt ccc atg tca acg				691
Val Glu Thr Tyr Thr Pro Glu Leu Leu Arg Asn Leu Pro Met Ser Thr				
185		190	195	
acc tcc act ggc cac aat ttc gca gag ctt ttc cac aac gct ggc ctc				739
Thr Ser Thr Gly His Asn Phe Ala Glu Leu Phe His Asn Ala Gly Leu				
200		205	210	
aaa gaa gtc aca ttg aca ccc att gag ggg ctg gct gaa ctt gac cag				787
Lys Glu Val Thr Leu Thr Pro Ile Glu Gly Leu Ala Glu Leu Asp Gln				
215		220	225	
cga ttt ggc ctc tca cca ggg cat gag tcg act ccg cag ttc cta ttc				835
Arg Phe Gly Leu Ser Pro Gly His Glu Ser Thr Pro Gln Phe Leu Phe				
230		235	240	245
agg gga att aaa tcc agt tagtgctgtt ttaagcggtc gag				876
Arg Gly Ile Lys Ser Ser				
250				

<210> 892

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 892

Val Thr Ser Pro Glu Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly			
1	5	10	15
Arg Ala Glu Ala Tyr His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln			
20		25	30
Phe Glu Arg Pro Ile Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile			
35		40	45
Val Ser Glu Glu Ala Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly			
50		55	60
Tyr Val Thr His Leu Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val			
65		70	75
Asp Gly Ser Glu Glu Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu			
85		90	95
Arg Arg Ser Thr Gly Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala			
100		105	110
His Asp Pro Glu Phe Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg			
115		120	125
Tyr Val Leu Trp Thr Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp			
130		135	140
Val Ser Leu Leu Lys Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala			

145	150	155	160
Trp Tyr Pro Lys Gly Ile Asp Ala Gly Thr Glu Val Asp Ser Val Asp			
	165	170	175
Gly Pro Ser Ala Phe Val Glu Thr Tyr Thr Pro Glu Leu Leu Arg Asn			
	180	185	190
Leu Pro Met Ser Thr Thr Ser Thr Gly His Asn Phe Ala Glu Leu Phe			
	195	200	205
His Asn Ala Gly Leu Lys Glu Val Thr Leu Thr Pro Ile Glu Gly Leu			
	210	215	220
Ala Glu Leu Asp Gln Arg Phe Gly Leu Ser Pro Gly His Glu Ser Thr			
	225	230	235
Pro Gln Phe Leu Phe Arg Gly Ile Lys Ser Ser			
	245	250	

<210> 893
 <211> 585
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(562)
 <223> RXS00998

<400> 893
 aatcggccta aaaggtgtga ccatttgggg gtagtggcga ttttaccagg tcacaggagg 60
 tgaaaatcca accatttttag gccgactaga gtaattaatt atg act tcc cgc gat 115
 Met Thr Ser Arg Asp
 1 5
 gat caa ccc caa gat ctg ctt tcg ctt gca gaa ctt gcc gcc acc aga 163
 Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu Leu Ala Ala Thr Arg
 10 15 20
 gct tta acc aca gac gaa ctt gaa gca ctc aac aac gcc aat tat ggc 211
 Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn Asn Ala Asn Tyr Gly
 25 30 35
 ctc gac cgc aat ctg ggg ctg cgc tac acc acc atc gag ccc ggc cgg 259
 Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr Ile Glu Pro Gly Arg
 40 45 50
 gtg gtc agc gaa ctt cac gtg gca tcc aag cac ctg caa gtg gtg ggc 307
 Val Val Ser Glu Leu His Val Ala Ser Lys His Leu Gln Val Val Gly
 55 60 65
 ttg gtc aac ggt ggt gtc tac gcc gcc atc gcc gaa tcc act gga tca 355
 Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala Glu Ser Thr Gly Ser
 70 75 80 85
 gtc gcc agc atg att tcc gcc cct gga aaa atg gtc gtc ggc atc aac 403
 Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met Val Val Gly Ile Asn
 90 95 100

aac aac acc gac ttc att tct gct gtg agc tcc ggt gtc atc gtg gcc 451
 Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser Gly Val Ile Val Ala
 105 110 115

gaa gca acg ccg att cag cta ggt ggc cgc acc cat ctg tgg cag atc 499
 Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr His Leu Trp Gln Ile
 120 125 130

gaa tgc acc cac cgc gga gaa gtc gtc gca cga acc aca ctg cgc acc 547
 Glu Cys Thr His Arg Gly Glu Val Val Ala Arg Thr Thr Leu Arg Thr
 135 140 145

atg gtg ctg aac aag tagccctata ctcgggcacc atg 585
 Met Val Leu Asn Lys
 150

<210> 894

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 894

Met Thr Ser Arg Asp Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu
 1 5 10 15

Leu Ala Ala Thr Arg Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn
 20 25 30

Asn Ala Asn Tyr Gly Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr
 35 40 45

Ile Glu Pro Gly Arg Val Val Ser Glu Leu His Val Ala Ser Lys His
 50 55 60

Leu Gln Val Val Gly Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala
 65 70 75 80

Glu Ser Thr Gly Ser Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met
 85 90 95

Val Val Gly Ile Asn Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser
 100 105 110

Gly Val Ile Val Ala Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr
 115 120 125

His Leu Trp Gln Ile Glu Cys Thr His Arg Gly Glu Val Val Ala Arg
 130 135 140

Thr Thr Leu Arg Thr Met Val Leu Asn Lys
 145 150

<210> 895

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1075)

<223> RXA01215

<400> 895

```

tcgaaggctg ggtgcaaaag aagcgccctg gaaccgctgc agcacaagcc gcagaagccg 60

cccaaaacgt ccacaaccag gaaggctaag caggatcctc atg act gct cac tgg 115
                                         Met Thr Ala His Trp
                                         1           5

aaa caa aac caa aag aac ctc atg ctg ttt tcg ggt cgt gcg cac cca 163
Lys Gln Asn Gln Lys Asn Leu Met Leu Phe Ser Gly Arg Ala His Pro
                        10                        15                        20

gaa ctg gca gaa gct gta gct aaa gag ctc gac gtc aac gtc acc cca 211
Glu Leu Ala Glu Ala Val Ala Lys Glu Leu Asp Val Asn Val Thr Pro
                        25                        30                        35

atg acg gca cgc gat ttc gcc aac ggt gaa atc tac gtc cgc ttc gag 259
Met Thr Ala Arg Asp Phe Ala Asn Gly Glu Ile Tyr Val Arg Phe Glu
                        40                        45                        50

gaa tca gtt cgt ggc tcc gac tgc ttc gtc ctg cag tcc cac acc cag 307
Glu Ser Val Arg Gly Ser Asp Cys Phe Val Leu Gln Ser His Thr Gln
                        55                        60                        65

cct ctc aac aag tgg ctc atg gaa cag ctg ctg atg atc gac gct ttg 355
Pro Leu Asn Lys Trp Leu Met Glu Gln Leu Leu Met Ile Asp Ala Leu
                        70                        75                        80                        85

aag cgt ggt tcc gca aag cgc atc acc gcg atc ctg ccg ttc tac cca 403
Lys Arg Gly Ser Ala Lys Arg Ile Thr Ala Ile Leu Pro Phe Tyr Pro
                        90                        95                        100

tat gcc cgc cag gac aag aag cac cgc ggc cgc gag cca att tct gct 451
Tyr Ala Arg Gln Asp Lys Lys His Arg Gly Arg Glu Pro Ile Ser Ala
                        105                        110                        115

cgc ctc atc gcc gac ctc atg ctc acc gct ggc gcg gac cgt atc gtg 499
Arg Leu Ile Ala Asp Leu Met Leu Thr Ala Gly Ala Asp Arg Ile Val
                        120                        125                        130

tcc gtg gac ttg cac acc gat cag atc cag ggc ttc ttc gac ggc cca 547
Ser Val Asp Leu His Thr Asp Gln Ile Gln Gly Phe Phe Asp Gly Pro
                        135                        140                        145

gtc gat cac atg cac gcc atg ccg atc ctc acc gat cac atc aag gaa 595
Val Asp His Met His Ala Met Pro Ile Leu Thr Asp His Ile Lys Glu
                        150                        155                        160                        165

aac tac aac ctg gac aac atc tgc gtg gtc tcc cct gac gca ggt cgc 643
Asn Tyr Asn Leu Asp Asn Ile Cys Val Val Ser Pro Asp Ala Gly Arg
                        170                        175                        180

gtg aag gtt gca gag aag tgg gct aac acc ttg ggc gat gcc cca atg 691
Val Lys Val Ala Glu Lys Trp Ala Asn Thr Leu Gly Asp Ala Pro Met
                        185                        190                        195

gcg ttc gtg cac aag acc cgc tcc acc gag gta gca aac cag gtt gtc 739
Ala Phe Val His Lys Thr Arg Ser Thr Glu Val Ala Asn Gln Val Val

```

200	205	210	
gcc aac cgc gtc gtc ggt gac gtc gac ggc aag gac tgc gtg ctt ctc			787
Ala Asn Arg Val Val Gly Asp Val Asp Gly Lys Asp Cys Val Leu Leu			
215	220	225	
gac gac atg atc gac act ggc ggc acc atc gcc ggc gct gtg ggc gtc			835
Asp Asp Met Ile Asp Thr Gly Gly Thr Ile Ala Gly Ala Val Gly Val			
230	235	240	245
ctg aag aag gct ggc gca aag tca gtc gtc atc gcc tgc acc cac ggt			883
Leu Lys Lys Ala Gly Ala Lys Ser Val Val Ile Ala Cys Thr His Gly			
250	255	260	
gtg ttc tct gac cca gcc cgc gag cgc ctg tct gca tgc ggt gct gaa			931
Val Phe Ser Asp Pro Ala Arg Glu Arg Leu Ser Ala Cys Gly Ala Glu			
265	270	275	
gaa gtc atc acc acc gac acc ctg cca cag tcc acc gag ggc tgg agc			979
Glu Val Ile Thr Thr Asp Thr Leu Pro Gln Ser Thr Glu Gly Trp Ser			
280	285	290	
aac ctg acc gtt ttg tcg atc gca ccg ctg ctg gct cgc acc atc aac			
1027			
Asn Leu Thr Val Leu Ser Ile Ala Pro Leu Leu Ala Arg Thr Ile Asn			
295	300	305	
gag atc ttc gaa aac ggt tcc gtc acc acc ctc ttc gag ggc gag gcc			
1075			
Glu Ile Phe Glu Asn Gly Ser Val Thr Thr Leu Phe Glu Gly Glu Ala			
310	315	320	325
taaacaccca tgcccaccac gga			
1098			

<210> 896
 <211> 325
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 896
 Met Thr Ala His Trp Lys Gln Asn Gln Lys Asn Leu Met Leu Phe Ser
 1 5 10 15
 Gly Arg Ala His Pro Glu Leu Ala Glu Ala Val Ala Lys Glu Leu Asp
 20 25 30
 Val Asn Val Thr Pro Met Thr Ala Arg Asp Phe Ala Asn Gly Glu Ile
 35 40 45
 Tyr Val Arg Phe Glu Glu Ser Val Arg Gly Ser Asp Cys Phe Val Leu
 50 55 60
 Gln Ser His Thr Gln Pro Leu Asn Lys Trp Leu Met Glu Gln Leu Leu
 65 70 75 80
 Met Ile Asp Ala Leu Lys Arg Gly Ser Ala Lys Arg Ile Thr Ala Ile
 85 90 95
 Leu Pro Phe Tyr Pro Tyr Ala Arg Gln Asp Lys Lys His Arg Gly Arg

100	105	110
Glu Pro Ile Ser Ala Arg Leu Ile Ala Asp Leu Met Leu Thr Ala Gly 115 120 125		
Ala Asp Arg Ile Val Ser Val Asp Leu His Thr Asp Gln Ile Gln Gly 130 135 140		
Phe Phe Asp Gly Pro Val Asp His Met His Ala Met Pro Ile Leu Thr 145 150 155 160		
Asp His Ile Lys Glu Asn Tyr Asn Leu Asp Asn Ile Cys Val Val Ser 165 170 175		
Pro Asp Ala Gly Arg Val Lys Val Ala Glu Lys Trp Ala Asn Thr Leu 180 185 190		
Gly Asp Ala Pro Met Ala Phe Val His Lys Thr Arg Ser Thr Glu Val 195 200 205		
Ala Asn Gln Val Val Ala Asn Arg Val Val Gly Asp Val Asp Gly Lys 210 215 220		
Asp Cys Val Leu Leu Asp Asp Met Ile Asp Thr Gly Gly Thr Ile Ala 225 230 235 240		
Gly Ala Val Gly Val Leu Lys Lys Ala Gly Ala Lys Ser Val Val Ile 245 250 255		
Ala Cys Thr His Gly Val Phe Ser Asp Pro Ala Arg Glu Arg Leu Ser 260 265 270		
Ala Cys Gly Ala Glu Glu Val Ile Thr Thr Asp Thr Leu Pro Gln Ser 275 280 285		
Thr Glu Gly Trp Ser Asn Leu Thr Val Leu Ser Ile Ala Pro Leu Leu 290 295 300		
Ala Arg Thr Ile Asn Glu Ile Phe Glu Asn Gly Ser Val Thr Thr Leu 305 310 315 320		
Phe Glu Gly Glu Ala 325		

<210> 897
 <211> 1470
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1447)
 <223> RXN00558

<400> 897
 gaacaggcac cgcaggaaga atgcggcggtt ttcggcggtt gggcgccagg tgaggaagtc 60

tcgaaactta cctactttgg cctcttcgca cttcagcacc gtg gtc aag aag ccc 115
 Val Val Lys Lys Pro
 1 5

gcg ggc atc gca gta ggc gat ggc gaa cag atc ctg gtt ttc aaa gat	163
Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile Leu Val Phe Lys Asp	
10 15 20	
ttg ggc cta gtc tcc caa gtt ttc gac caa cca att ctg gaa tcc ctc	211
Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro Ile Leu Glu Ser Leu	
25 30 35	
cgc gga aac atc gcc atc gga cac acc cga tac acc acc gcc ggc gga	259
Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr Thr Thr Ala Gly Gly	
40 45 50	
aac acc tgg gaa aat gcc cag cct atg ttc cgc atg gca cca gat ggc	307
Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg Met Ala Pro Asp Gly	
55 60 65	
acc gat atc gcc ctt gga cac aac ggc aac ctg att aat tac atc gag	355
Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu Ile Asn Tyr Ile Glu	
70 75 80 85	
ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc gat ccc gcc aag aag	403
Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val Asp Pro Ala Lys Lys	
90 95 100	
cca tca gat acc gat gtg ctc act gga ctg ctc gca agc ggc gtc cat	451
Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu Ala Ser Gly Val His	
105 110 115	
gac gga aat aat ctc ttt gat tcc gcc aag gaa ctc ctc ccc agc gtc	499
Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu Leu Leu Pro Ser Val	
120 125 130	
aag gga gcc tac tgc ctc acc ttc acc gac gga cac acc ctg tac gca	547
Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly His Thr Leu Tyr Ala	
135 140 145	
gcg cgt gat cca ttc ggc atc cgc cca ctg tcc atc ggc cgc ctc gag	595
Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser Ile Gly Arg Leu Glu	
150 155 160 165	
cgc ggc tgg gta gtc gca tct gaa acc gca ggc ctc gac atc gta ggt	643
Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala Leu Asp Ile Val Gly	
170 175 180	
gcc tgc cat gtg cgc gag gtc gaa cca ggc gaa ctg att gct atc gac	691
Ala Ser His Val Arg Glu Val Glu Pro Gly Glu Leu Ile Ala Ile Asp	
185 190 195	
gaa tcc ggc ctc aag tcc gca cga ttc gcc gag aca acc cgc aaa ggt	739
Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu Thr Thr Arg Lys Gly	
200 205 210	
tgc gtc ttc gaa tac gtt tac ctg gct cgt cca gac tcc gtg atc aag	787
Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro Asp Ser Val Ile Lys	
215 220 225	
gga aga aac gtc aac gaa gcc cga ctt gaa atc ggc cgc aag ctc gct	835
Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile Gly Arg Lys Leu Ala	
230 235 240 245	

gca gaa gca cca gca gtc ggc gat cta gtc atc cca acc cca gaa tca 883
 Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile Pro Thr Pro Glu Ser
 250 255 260

ggc acc cca gca gca gtt gga ttc gcc caa gca tct ggc atc cca ttc 931
 Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala Ser Gly Ile Pro Phe
 265 270 275

ggc caa ggc atg gtc aaa aac gcc tac gtt ggc cga acc ttc atc cag 979
 Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly Arg Thr Phe Ile Gln
 280 285 290

cct tcc gac act ctc cgc caa ctg gga atc cgc ctc aag ctg aac cca
 1027
 Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg Leu Lys Leu Asn Pro
 295 300 305

ttg cgc gag gtt atc gcc gga aag cgc ctt gtg gtt gtg gat gat tcc
 1075
 Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val Val Val Asp Asp Ser
 310 315 320 325

atc gtc cgc ggt aac acc caa cgc gcc gtg atc cgc atg ttg cgc gaa
 1123
 Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile Arg Met Leu Arg Glu
 330 335 340

gcc ggt gca gct gag gtt cac gta cgc atc gcc tca cca ccc gtg aaa
 1171
 Ala Gly Ala Ala Glu Val His Val Arg Ile Ala Ser Pro Pro Val Lys
 345 350 355

tgg cca tgc ttc tac ggc atc gat ttt gcc acc cca ggc gaa ctc att
 1219
 Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr Pro Gly Glu Leu Ile
 360 365 370

gcc aac gct gtc acc agt gac aac gaa gca gaa atg gta gaa gca gtc
 1267
 Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu Met Val Glu Ala Val
 375 380 385

cgc tcc gca atc ggc gca gac acc ctc ggc tac gtc tcc atc gac tcc
 1315
 Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr Val Ser Ile Asp Ser
 390 395 400 405

atg gtt gca gca acc gag caa cca gcc aac gaa ctc tgc atc gcc tgc
 1363
 Met Val Ala Ala Thr Glu Gln Pro Ala Asn Glu Leu Cys Ile Ala Cys
 410 415 420

ttc gac ggc aaa tac ccc atg ggt ctg cca cag gga aac agc aac gca
 1411
 Phe Asp Gly Lys Tyr Pro Met Gly Leu Pro Gln Gly Asn Ser Asn Ala
 425 430 435

gac cta gtc cgc aag atg caa gca acc gcc tca agt taagatcggt
 1457
 Asp Leu Val Arg Lys Met Gln Ala Thr Ala Ser Ser
 440 445

aggcgatagg ggt
1470

<210> 898
<211> 449
<212> PRT
<213> Corynebacterium glutamicum

<400> 898
Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile
1 5 10 15
Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro
20 25 30
Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr
35 40 45
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg
50 55 60
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu
65 70 75 80
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val
85 90 95
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu
100 105 110
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu
115 120 125
Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly
130 135 140
His Thr Leu Tyr Ala Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser
145 150 155 160
Ile Gly Arg Leu Glu Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala
165 170 175
Leu Asp Ile Val Gly Ala Ser His Val Arg Glu Val Glu Pro Gly Glu
180 185 190
Leu Ile Ala Ile Asp Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu
195 200 205
Thr Thr Arg Lys Gly Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro
210 215 220
Asp Ser Val Ile Lys Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile
225 230 235 240
Gly Arg Lys Leu Ala Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile
245 250 255
Pro Thr Pro Glu Ser Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala
260 265 270

Ser Gly Ile Pro Phe Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly
 275 280 285
 Arg Thr Phe Ile Gln Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg
 290 295 300
 Leu Lys Leu Asn Pro Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val
 305 310 315 320
 Val Val Asp Asp Ser Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile
 325 330 335
 Arg Met Leu Arg Glu Ala Gly Ala Ala Glu Val His Val Arg Ile Ala
 340 345 350
 Ser Pro Pro Val Lys Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr
 355 360 365
 Pro Gly Glu Leu Ile Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu
 370 375 380
 Met Val Glu Ala Val Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr
 385 390 395 400
 Val Ser Ile Asp Ser Met Val Ala Ala Thr Glu Gln Pro Ala Asn Glu
 405 410 415
 Leu Cys Ile Ala Cys Phe Asp Gly Lys Tyr Pro Met Gly Leu Pro Gln
 420 425 430
 Gly Asn Ser Asn Ala Asp Leu Val Arg Lys Met Gln Ala Thr Ala Ser
 435 440 445
 Ser

<210> 899
 <211> 524
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (61)..(501)
 <223> FRXA00558

<400> 899
 gggcgccagg tgaggaagta tcgcagctca cctactttgg cctcttcgca gttcagcacc 60
 gtg gtc aag aag ccc gcg ggc atc gca gta ggc gat ggc gaa cag atc 108
 Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile
 1 5 10 15
 ctg gtt ttc aaa gat ttg ggc cta gtc tcc caa gtt ttc gac caa cca 156
 Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro
 20 25 30
 att ctg gaa tcc ctc cgc gga aac atc gcc atc gga cac acc cga tac 204
 Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr

35	40	45	
acc acc gcc ggc gga aac acc tgg gaa aat gcc cag cct atg ttc cgc			252
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg			
50	55	60	
atg gca cca gat ggc acc gat atc gcc ctt gga cac aac ggc aac ctg			300
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu			
65	70	75	80
att aat tac atc gag ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc			348
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val			
85	90	95	
gat ccc gcc aag aag cca tca gat acc gat gtg ctc act gga ctg ctc			396
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu			
100	105	110	
gca agc ggc gtc cat gac gga aat aat ctc ttt gat tcc gcc aag gaa			444
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu			
115	120	125	
ctc ctc ccc agc gtc aag gga gcc tac tgc ctc acc ttc acc gac gga			492
Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly			
130	135	140	
cac acc ctg taagcagcgc gtgatccatt cgg			524
His Thr Leu			
145			

<210> 900

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 900

Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile			
1	5	10	15
Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro			
20	25	30	
Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr			
35	40	45	
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg			
50	55	60	
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu			
65	70	75	80
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val			
85	90	95	
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu			
100	105	110	
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu			
115	120	125	

Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly
 130 135 140

His Thr Leu
 145

<210> 901

<211> 1386

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1363)

<223> RXN00626

<400> 901

tcattttaag gcgcttttcg acgccacttt caaccatttc cgaaccgccca agaatactgg 60

aatagcttgg atcaagtttt gcaggataaa ctgtgcaacc atg cgc att ctg gta 115
 Met Arg Ile Leu Val
 1 5

atc ggc tcg ggc gcc cgt gag cac gcc ctc ctc cgt gga ctg tca act 163
 Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr
 10 15 20

gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt 211
 Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu
 25 30 35

gga tcg atc gca act gtc cac cct ggc atc aag gct gat gat cca gag 259
 Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu
 40 45 50

gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc 307
 Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile
 55 60 65

ggc cca gag atc cct ttg gtt gcg ggt gtt gct gat gca ctt cgc gcg 355
 Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala Asp Ala Leu Arg Ala
 70 75 80 85

gcg ggt atc gct gtg ttt ggt cct aac aag gac gct gct cgt atc gag 403
 Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp Ala Ala Arg Ile Glu
 90 95 100

ggc tcc aag gct ttc gct aag gat gtc atg gct gcg cag ggt gtt cgt 451
 Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala Ala Gln Gly Val Arg
 105 110 115

act gct cat gct gag act att act cct ggt gcg tct tct gaa gat att 499
 Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala Ser Ser Glu Asp Ile
 120 125 130

gat gct gcc ata gat cgt ttc ggc cca acg tgg gtt gtc aag gat gat 547
 Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp Val Val Lys Asp Asp
 135 140 145

ggc ttg tct gcg ggc aag ggt gtt gtg gtt acc ccc gat cgt gca gca 595

Gly Leu Ser Ala Gly Lys Gly Val Val Val Thr Pro Asp Arg Ala Ala
 150 155 160 165

gca cgt gct cac gta gat gca gtg ctt gag ggc gga aat cca gtt ttg 643
 Ala Arg Ala His Val Asp Ala Val Leu Glu Gly Gly Asn Pro Val Leu
 170 175 180

ctg gag tcc ttc ctt gat ggc cct gag gtt tcc ctg ttc tgc ctg gtt 691
 Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser Leu Phe Cys Leu Val
 185 190 195

gat ggc gag acg gta gtt cct ctg ctg cca gcg cag gat cac aag cgt 739
 Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln Asp His Lys Arg
 200 205 210

gcg tac gac aac gat gag ggc cca aac act ggt ggc atg ggt gct tat 787
 Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly Met Gly Ala Tyr
 215 220 225

gcg ccg ctt cct tgg ctg cct gaa gat ggc gtc cag cgc att gtc gat 835
 Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln Arg Ile Val Asp
 230 235 240 245

gag gtc tgc gtt cct gtt gct cgt gag atg gtg gca cgt ggt tgc gcg 883
 Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala Arg Gly Cys Ala
 250 255 260

tac tcc ggt ctg ctt tac gca ggt atc gca tgg ggt gca gaa ggc cct 931
 Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly Ala Glu Gly Pro
 265 270 275

gca gta gtg gag ttc aac tgc cgc ttc ggc gat cca gaa acc cag gct 979
 Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro Glu Thr Gln Ala
 280 285 290

gta ctg gca cta ctg aag act cct cta gca gta ctg ctc aac gca gtt
 1027
 Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu Leu Asn Ala Val
 295 300 305

gct act gga acc ttg gca gag cag cca gca ctg gag tgg gag gat gct
 1075
 Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu Trp Glu Asp Ala
 310 315 320 325

tac gcc ctg act gtg gtg ttg gct tct tac aac tac cca gag gca cct
 1123
 Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr Pro Glu Ala Pro
 330 335 340

cgt act ggt gat gtc atc cgc aac gct gat gca gat aac gtt ctt cac
 1171
 Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp Asn Val Leu His
 345 350 355

gct ggt acc gca ctc aat gct gaa ggc gag ctg gtc tct gcg ggc ggt
 1219
 Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val Ser Ala Gly Gly
 360 365 370

cgt gtt ctt aac gtg atc ggt gtg ggt gag acc ctg gag gct gca cgc
1267

Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu Glu Ala Ala Arg
375 380 385

gat aac gcg tac acc acc atc aag gac att gaa ctt gag gga agc cac
1315

Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu Glu Gly Ser His
390 395 400 405

tac cgc agc gat atc gca ttg gct gca tta gag ggt cgt atc tcg atc
1363

Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly Arg Ile Ser Ile
410 415 420

taaaagcagt acgcagatag gct
1386

<210> 902

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 902

Met Arg Ile Leu Val Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu
1 5 10 15

Arg Gly Leu Ser Thr Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro
20 25 30

Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys
35 40 45

Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser
50 55 60

Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala
65 70 75 80

Asp Ala Leu Arg Ala Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp
85 90 95

Ala Ala Arg Ile Glu Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala
100 105 110

Ala Gln Gly Val Arg Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala
115 120 125

Ser Ser Glu Asp Ile Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp
130 135 140

Val Val Lys Asp Asp Gly Leu Ser Ala Gly Lys Gly Val Val Val Thr
145 150 155 160

Pro Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly
165 170 175

Gly Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser
180 185 190

Leu Phe Cys Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala
195 200 205

Gln Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly
210 215 220

Gly Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val
225 230 235 240

Gln Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val
245 250 255

Ala Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp
260 265 270

Gly Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp
275 280 285

Pro Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val
290 295 300

Leu Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu
305 310 315 320

Glu Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn
325 330 335

Tyr Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala
340 345 350

Asp Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu
355 360 365

Val Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr
370 375 380

Leu Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu
385 390 395 400

Leu Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu
405 410 415

Gly Arg Ile Ser Ile
420

<210> 903

<211> 364

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(364)

<223> FRXA00629

<400> 903

tcattttaag gcgcttttcg acgccacttt caaccatttc cgaaccgccca agaatactgg 60

aatagcttgg atcaagtttt gcaggataaa ctgtgcaacc atg cgc att ctg gta 115
Met Arg Ile Leu Val

	1	5	
atc ggc tcg ggc gcc cgt gag cac gcc ctc ctc cgt gga ctg tca act			163
Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr			
	10	15	20
gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt			211
Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu			
	25	30	35
gga tcg atc gca act gtc cac cct ggc atc aag gct gat gat cca gag			259
Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu			
	40	45	50
gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc			307
Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile			
	55	60	65
ggc cca gag atc cct ttg gtt gcg ggt gtt gct gat gca ctt cgc gcg			355
Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala Asp Ala Leu Arg Ala			
	70	75	80
gcg ggt atc			364
Ala Gly Ile			

<210> 904

<211> 88

<212> PRT

<213> Corynebacterium glutamicum

<400> 904

Met Arg Ile Leu Val Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu
1 5 10 15

Arg Gly Leu Ser Thr Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro
20 25 30

Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys
35 40 45

Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser
50 55 60

Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala
65 70 75 80

Asp Ala Leu Arg Ala Ala Gly Ile
85

<210> 905

<211> 803

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(780)

<223> FRXA00626

<400> 905

gat cgt gca gca gca cgt gct cac gta gat gca gtg ctt gag ggc gga	48
Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly Gly	
1 5 10 15	
aat cca gtt ttg ctg gag tcc ttc ctt gat ggc cct gag gtt tcc ctg	96
Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser Leu	
20 25 30	
ttc ttc ctg gtt gat ggc gag acg gta gtt cct ctg ctg cca gcg cag	144
Phe Phe Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln	
35 40 45	
gat cac aag cgt gcg tac gac aac gat gag ggc cca aac act ggt ggc	192
Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly	
50 55 60	
atg ggt gct tat gcg ccg ctt cct tgg ctg cct gaa gat ggc gtc cag	240
Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln	
65 70 75 80	
cgc att gtc gat gag gtc tgc gtt cct gtt gct cgt gag atg gtg gca	288
Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala	
85 90 95	
cgt ggt tgc gcg tac tcc ggt ctg ctt tac gca ggt atc gca tgg ggt	336
Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly	
100 105 110	
gca gaa ggc cct gca gta gtg gag ttc aac tgc cgc ttc ggc gat cca	384
Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro	
115 120 125	
gaa acc cag gct gta ctg gca cta ctg aag act cct cta gca gta ctg	432
Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu	
130 135 140	
ctc aac gca gtt gct act gga acc ttg gca gag cag cca gca ctg gag	480
Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu	
145 150 155 160	
tgg gag gat gct tac gcc ctg act gtg gtg ttg gct tct tac aac tac	528
Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr	
165 170 175	
cca gag gca cct cgt act ggt gat gtc atc cgc aac gct gat gca gat	576
Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp	
180 185 190	
aac gtt ctt cac gct ggt acc gca ctc aat gct gaa ggc gag ctg gtc	624
Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val	
195 200 205	
tct gcg ggc ggt cgt gtt ctt aac gtg atc ggt gtg ggt gag acc ctg	672
Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu	
210 215 220	
gag gct gca cgc gat aac gcg tac acc acc atc aag gac att gaa ctt	720
Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu	
225 230 235 240	

gag gga agc cac tac cgc agc gat atc gca ttg gct gca tta gag ggt 768
 Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly
 245 250 255

cgt atc tcg atc taaaagcagt acgcagatag gct 803
 Arg Ile Ser Ile
 260

<210> 906

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 906

Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly Gly
 1 5 10 15

Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser Leu
 20 25 30

Phe Phe Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln
 35 40 45

Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly
 50 55 60

Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln
 65 70 75 80

Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala
 85 90 95

Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly
 100 105 110

Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro
 115 120 125

Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu
 130 135 140

Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu
 145 150 155 160

Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr
 165 170 175

Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp
 180 185 190

Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val
 195 200 205

Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu
 210 215 220

Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu
 225 230 235 240

Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly
 245 250 255

Arg Ile Ser Ile
 260

<210> 907
 <211> 714
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(691)
 <223> RXA02623

<400> 907
 aatcctgaag aggaagaatc cgacgaagaa attgagacag aaactgaggc tgaagaaacc 60
 aatgatgggtt ccgaggccga agaccgttaa catatctgtt gtg aat tct gac tct 115
 Val Asn Ser Asp Ser
 1 5
 acg acc acc att gtc gtg cta gct tcc gga aca ggc acc ctc ctt cag 163
 Thr Thr Thr Ile Val Val Leu Ala Ser Gly Thr Gly Thr Leu Leu Gln
 10 15 20
 tca ctc att gaa gcg caa ggt acc tat tcg atc gtg ggc gtt gtc tct 211
 Ser Leu Ile Glu Ala Gln Gly Thr Tyr Ser Ile Val Gly Val Val Ser
 25 30 35
 gac gtc gaa tgc cct gca ctt tcc aga gcc gca gat gca ggt att gat 259
 Asp Val Glu Cys Pro Ala Leu Ser Arg Ala Ala Asp Ala Gly Ile Asp
 40 45 50
 act gca gtt gtt ccg ctt gga aaa gat cgt gca cag tgg aac cac gag 307
 Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala Gln Trp Asn His Glu
 55 60 65
 ctt gca gac gca gtt gca gta agc gac cca gat ttg gtg gtc tct gcg 355
 Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp Leu Val Val Ser Ala
 70 75 80 85
 gga ttc atg aaa att ttg ggc gaa ggt ttc ctc tca agg ttc ccg tcc 403
 Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu Ser Arg Phe Pro Ser
 90 95 100
 cgc atc atc aac acc cac cca gct tta ttg cct tct ttc cct ggt gcc 451
 Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro Ser Phe Pro Gly Ala
 105 110 115
 cac gcg gtt cgc gat gct ttg gca tac ggt gtg aaa gtg tca ggt tcg 499
 His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val Lys Val Ser Gly Ser
 120 125 130
 aca gtt cac ctt gtc gat gct ggt gtg gat acc ggc cca att att gct 547
 Thr Val His Leu Val Asp Ala Gly Val Asp Thr Gly Pro Ile Ile Ala
 135 140 145
 caa cga gca gtg ccg gta gaa gtg aat gat gat gaa tcc agc ctg cat 595

Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp Glu Ser Ser Leu His
 150 155 160 165

gaa aga atc aag cag gtt gag cgt aaa ctc att gta gaa gtc ctg aac 643
 Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile Val Glu Val Leu Asn
 170 175 180

agc gtg gaa ttt tcg cgt cag ggt ggc gta caa ctc aac tgg aga ggc 691
 Ser Val Glu Phe Ser Arg Gln Gly Gly Val Gln Leu Asn Trp Arg Gly
 185 190 195

taaatccttc atgagcgatg atc 714

<210> 908

<211> 197

<212> PRT

<213> Corynebacterium glutamicum

<400> 908

Val Asn Ser Asp Ser Thr Thr Thr Ile Val Val Leu Ala Ser Gly Thr
 1 5 10 15

Gly Thr Leu Leu Gln Ser Leu Ile Glu Ala Gln Gly Thr Tyr Ser Ile
 20 25 30

Val Gly Val Val Ser Asp Val Glu Cys Pro Ala Leu Ser Arg Ala Ala
 35 40 45

Asp Ala Gly Ile Asp Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala
 50 55 60

Gln Trp Asn His Glu Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp
 65 70 75 80

Leu Val Val Ser Ala Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu
 85 90 95

Ser Arg Phe Pro Ser Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro
 100 105 110

Ser Phe Pro Gly Ala His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val
 115 120 125

Lys Val Ser Gly Ser Thr Val His Leu Val Asp Ala Gly Val Asp Thr
 130 135 140

Gly Pro Ile Ile Ala Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp
 145 150 155 160

Glu Ser Ser Leu His Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile
 165 170 175

Val Glu Val Leu Asn Ser Val Glu Phe Ser Arg Gln Gly Gly Val Gln
 180 185 190

Leu Asn Trp Arg Gly
 195

<210> 909

<211> 1347
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1324)
 <223> RXA01442

<400> 909

```

aattaagcaa cctttttaac aggttttagag ctttcacgag gtggcgtcag ataaagttaa 60

caccaatatt tctgacatct tccaacggag gctaaaaggc atg tac atc cca gag 115
                                         Met Tyr Ile Pro Glu
                                         1           5

tcg atc ggc acc cct ttg acc ccc aat gcc acg aaa gtg atg ctg ctg 163
Ser Ile Gly Thr Pro Leu Thr Pro Asn Ala Thr Lys Val Met Leu Leu
                        10                      15                      20

gga tca gga gaa tta ggc aaa gaa gta gcc atc gct ttc cag cgt ctc 211
Gly Ser Gly Glu Leu Gly Lys Glu Val Ala Ile Ala Phe Gln Arg Leu
                        25                      30                      35

ggc ctg gaa gtc cat gca gtt gat cgc tac gaa cat gcc cca gcc cac 259
Gly Leu Glu Val His Ala Val Asp Arg Tyr Glu His Ala Pro Ala His
                        40                      45                      50

cag gtc gct cac ttc tcc tat gtc atc gac atg aca gat gca gcc cag 307
Gln Val Ala His Phe Ser Tyr Val Ile Asp Met Thr Asp Ala Ala Gln
                        55                      60                      65

gtg cgg gaa ttg gtg gag cgt gtg cgc cca gat ttt gtc att cct gaa 355
Val Arg Glu Leu Val Glu Arg Val Arg Pro Asp Phe Val Ile Pro Glu
                        70                      75                      80                      85

atc gaa gca ctg gca acc gat gaa ctg gtg aag atc gaa gaa gag ggg 403
Ile Glu Ala Leu Ala Thr Asp Glu Leu Val Lys Ile Glu Glu Glu Gly
                        90                      95                      100

cta gct acc atc gtg ccc act gca cgt gca gcc aag ctg acc atg aac 451
Leu Ala Thr Ile Val Pro Thr Ala Arg Ala Ala Lys Leu Thr Met Asn
                        105                      110                      115

cgc gaa ggc atc cgc aag ctg gcg gca gag gaa ctg ggt ctt cca acc 499
Arg Glu Gly Ile Arg Lys Leu Ala Ala Glu Glu Leu Gly Leu Pro Thr
                        120                      125                      130

tcc aac tat gag ttc tgc tcc act ttc gag gaa ttc tcc gca gct gct 547
Ser Asn Tyr Glu Phe Cys Ser Thr Phe Glu Glu Phe Ser Ala Ala Ala
                        135                      140                      145

gaa aag ctt ggt tac ccc aac gtg gtg aaa cca gtg atg agt tct tcc 595
Glu Lys Leu Gly Tyr Pro Asn Val Val Lys Pro Val Met Ser Ser Ser
                        150                      155                      160                      165

ggc aag ggc caa tct gtt ttg cgt agt tca gac gat ctg cag gca gca 643
Gly Lys Gly Gln Ser Val Leu Arg Ser Ser Asp Asp Leu Gln Ala Ala
                        170                      175                      180

tgg gat tat gcg atg agc ggt gca cgc gtg gcc aac tcc cgc gtc atc 691

```


Trp	Asp	Tyr	Ala	Met	Ser	Gly	Ala	Arg	Val	Ala	Asn	Ser	Arg	Val	Ile		
			185					190					195				
gtg	gaa	gct	ttc	gtg	gaa	ttc	gat	tac	gag	atc	acc	ctg	ttg	aca	gta	739	
Val	Glu	Ala	Phe	Val	Glu	Phe	Asp	Tyr	Glu	Ile	Thr	Leu	Leu	Thr	Val		
		200					205					210					
agg	tcc	atc	gat	ccc	acc	acc	tct	aag	cct	gcg	acc	tgg	ttc	tgt	gag	787	
Arg	Ser	Ile	Asp	Pro	Thr	Thr	Ser	Lys	Pro	Ala	Thr	Trp	Phe	Cys	Glu		
	215					220				225							
ccc	att	ggg	cac	cgc	caa	gaa	gac	ggc	gac	tac	gtg	gaa	tcc	tgg	cag	835	
Pro	Ile	Gly	His	Arg	Gln	Glu	Asp	Gly	Asp	Tyr	Val	Glu	Ser	Trp	Gln		
230				235					240						245		
cca	atg	gag	atg	act	cct	cgc	gcg	ctg	gaa	aac	gca	cgc	tca	gta	gcc	883	
Pro	Met	Glu	Met	Thr	Pro	Arg	Ala	Leu	Glu	Asn	Ala	Arg	Ser	Val	Ala		
			250					255						260			
gca	cgc	atc	acc	aac	gca	ttg	ggc	gga	cgc	ggc	gta	ttt	ggg	gtg	gag	931	
Ala	Arg	Ile	Thr	Asn	Ala	Leu	Gly	Gly	Arg	Gly	Val	Phe	Gly	Val	Glu		
		265					270						275				
ctc	ttt	gtc	tcc	ggc	gat	gac	gtg	tac	ttc	tct	gaa	gtc	tcc	cca	cgc	979	
Leu	Phe	Val	Ser	Gly	Asp	Asp	Val	Tyr	Phe	Ser	Glu	Val	Ser	Pro	Arg		
	280					285					290						
cca	cac	gac	acc	ggc	ctt	gtc	acc	ctt	gcc	acc	cag	cgt	ttc	tct	gaa		
1027																	
Pro	His	Asp	Thr	Gly	Leu	Val	Thr	Leu	Ala	Thr	Gln	Arg	Phe	Ser	Glu		
	295				300						305						
ttt	gaa	ctc	cac	gcc	aag	gca	att	ctg	gga	ttg	cct	ggt	gat	gtc	acc		
1075																	
Phe	Glu	Leu	His	Ala	Lys	Ala	Ile	Leu	Gly	Leu	Pro	Val	Asp	Val	Thr		
310				315				320					325				
ctg	att	tct	cca	ggt	gcc	tcc	gct	gtc	atc	tac	ggt	ggc	atc	gaa	tct		
1123																	
Leu	Ile	Ser	Pro	Gly	Ala	Ser	Ala	Val	Ile	Tyr	Gly	Gly	Ile	Glu	Ser		
				330				335					340				
gaa	ggc	gtg	agc	tac	acc	ggg	ttg	gct	gaa	gcg	ctg	cca	gtg	gct	gaa		
1171																	
Glu	Gly	Val	Ser	Tyr	Thr	Gly	Leu	Ala	Glu	Ala	Leu	Ala	Val	Ala	Glu		
		345					350						355				
act	gat	ctt	cgt	atc	ttt	gcc	aag	cca	gag	gcc	ttc	acc	aag	cgt	cgc		
1219																	
Thr	Asp	Leu	Arg	Ile	Phe	Ala	Lys	Pro	Glu	Ala	Phe	Thr	Lys	Arg	Arg		
	360					365					370						
atg	ggt	ggt	gca	gtg	tcc	acc	gct	gag	gat	gtg	gct	gca	gcc	agg	gac		
1267																	
Met	Gly	Val	Ala	Val	Ser	Thr	Ala	Glu	Asp	Val	Ala	Ala	Ala	Arg	Asp		
	375					380				385							
cgc	gcc	act	ttg	gct	gcc	gcg	gcg	atc	aag	ggt	cat	cca	gga	aat	tcc		
1315																	
Arg	Ala	Thr	Leu	Ala	Ala	Ala	Ala	Ile	Lys	Val	His	Pro	Gly	Asn	Ser		
390				395				400						405			

gca gag gct taacatgctg ggaaagcatc ggg
 1347
 Ala Glu Ala

<210> 910
 <211> 408
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 910
 Met Tyr Ile Pro Glu Ser Ile Gly Thr Pro Leu Thr Pro Asn Ala Thr
 1 5 10 15
 Lys Val Met Leu Leu Gly Ser Gly Glu Leu Gly Lys Glu Val Ala Ile
 20 25 30
 Ala Phe Gln Arg Leu Gly Leu Glu Val His Ala Val Asp Arg Tyr Glu
 35 40 45
 His Ala Pro Ala His Gln Val Ala His Phe Ser Tyr Val Ile Asp Met
 50 55 60
 Thr Asp Ala Ala Gln Val Arg Glu Leu Val Glu Arg Val Arg Pro Asp
 65 70 75 80
 Phe Val Ile Pro Glu Ile Glu Ala Leu Ala Thr Asp Glu Leu Val Lys
 85 90 95
 Ile Glu Glu Glu Gly Leu Ala Thr Ile Val Pro Thr Ala Arg Ala Ala
 100 105 110
 Lys Leu Thr Met Asn Arg Glu Gly Ile Arg Lys Leu Ala Ala Glu Glu
 115 120 125
 Leu Gly Leu Pro Thr Ser Asn Tyr Glu Phe Cys Ser Thr Phe Glu Glu
 130 135 140
 Phe Ser Ala Ala Ala Glu Lys Leu Gly Tyr Pro Asn Val Val Lys Pro
 145 150 155 160
 Val Met Ser Ser Ser Gly Lys Gly Gln Ser Val Leu Arg Ser Ser Asp
 165 170 175
 Asp Leu Gln Ala Ala Trp Asp Tyr Ala Met Ser Gly Ala Arg Val Ala
 180 185 190
 Asn Ser Arg Val Ile Val Glu Ala Phe Val Glu Phe Asp Tyr Glu Ile
 195 200 205
 Thr Leu Leu Thr Val Arg Ser Ile Asp Pro Thr Thr Ser Lys Pro Ala
 210 215 220
 Thr Trp Phe Cys Glu Pro Ile Gly His Arg Gln Glu Asp Gly Asp Tyr
 225 230 235 240
 Val Glu Ser Trp Gln Pro Met Glu Met Thr Pro Arg Ala Leu Glu Asn
 245 250 255

Ala Arg Ser Val Ala Ala Arg Ile Thr Asn Ala Leu Gly Gly Arg Gly
 260 265 270

Val Phe Gly Val Glu Leu Phe Val Ser Gly Asp Asp Val Tyr Phe Ser
 275 280 285

Glu Val Ser Pro Arg Pro His Asp Thr Gly Leu Val Thr Leu Ala Thr
 290 295 300

Gln Arg Phe Ser Glu Phe Glu Leu His Ala Lys Ala Ile Leu Gly Leu
 305 310 315 320

Pro Val Asp Val Thr Leu Ile Ser Pro Gly Ala Ser Ala Val Ile Tyr
 325 330 335

Gly Gly Ile Glu Ser Glu Gly Val Ser Tyr Thr Gly Leu Ala Glu Ala
 340 345 350

Leu Ala Val Ala Glu Thr Asp Leu Arg Ile Phe Ala Lys Pro Glu Ala
 355 360 365

Phe Thr Lys Arg Arg Met Gly Val Ala Val Ser Thr Ala Glu Asp Val
 370 375 380

Ala Ala Ala Arg Asp Arg Ala Thr Leu Ala Ala Ala Ile Lys Val
 385 390 395 400

His Pro Gly Asn Ser Ala Glu Ala
 405

<210> 911
 <211> 2409
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2386)
 <223> RXN00537

<400> 911
 acccggaaca tgccgtcgaa aagctaaccg gcccatctat tgatggccta gaggctttcc 60

tgtccgccgt tggcaccatc gcggcttaag aggagtaa atg agc act ttt gtc 115
 Met Ser Thr Phe Val
 1 5

aat gac acc gtc gaa gac gca atc aag acc cct gag ctg gat cag cca 163
 Asn Asp Thr Val Glu Asp Ala Ile Lys Thr Pro Glu Leu Asp Gln Pro
 10 15 20

ttt gag gct ctt ggt ctg aaa gac gac gag tac gcg cgc atc aag gaa 211
 Phe Glu Ala Leu Gly Leu Lys Asp Asp Glu Tyr Ala Arg Ile Lys Glu
 25 30 35

atc ctt ggc cgc cgc cca acc gac gcc gag ctg acc gtt tac tcc gtc 259
 Ile Leu Gly Arg Arg Pro Thr Asp Ala Glu Leu Thr Val Tyr Ser Val
 40 45 50

atg tgg tcg gag cac tgc tcc tac aag tcc tcc aag gtt cac ctg cgt 307

Met	Trp	Ser	Glu	His	Cys	Ser	Tyr	Lys	Ser	Ser	Lys	Val	His	Leu	Arg		
55						60					65						
tac	ttc	ggt	gaa	acc	acc	act	gag	gaa	atg	gct	tcc	aag	att	ctt	gcc	355	
Tyr	Phe	Gly	Glu	Thr	Thr	Thr	Glu	Glu	Met	Ala	Ser	Lys	Ile	Leu	Ala		
70					75				80						85		
ggc	atc	ggc	gag	aac	gct	ggt	gtg	gtc	gac	atc	gga	gac	ggc	aac	gcc	403	
Gly	Ile	Gly	Glu	Asn	Ala	Gly	Val	Val	Asp	Ile	Gly	Asp	Gly	Asn	Ala		
				90					95					100			
gtg	acc	ttc	cgc	gtg	gag	tcc	cac	aac	cac	cca	tcc	ttc	gta	gag	cca	451	
Val	Thr	Phe	Arg	Val	Glu	Ser	His	Asn	His	Pro	Ser	Phe	Val	Glu	Pro		
			105					110					115				
cac	cag	ggc	gct	gcg	acc	ggc	gtc	ggc	ggc	atc	gtc	cgc	gac	att	atg	499	
His	Gln	Gly	Ala	Ala	Thr	Gly	Val	Gly	Gly	Ile	Val	Arg	Asp	Ile	Met		
	120						125					130					
gct	atg	ggc	gca	cgc	cca	atc	gct	gtg	atg	gat	cag	ctg	cgt	ttc	ggt	547	
Ala	Met	Gly	Ala	Arg	Pro	Ile	Ala	Val	Met	Asp	Gln	Leu	Arg	Phe	Gly		
	135					140					145						
gca	ctg	gac	aac	cca	gac	acc	cag	cgt	gtg	ttt	cct	ggc	gtt	gtt	gac	595	
Ala	Leu	Asp	Asn	Pro	Asp	Thr	Gln	Arg	Val	Phe	Pro	Gly	Val	Val	Asp		
	150				155					160					165		
ggc	att	tcc	cat	tac	ggc	aac	tgc	ctc	ggc	ctg	cca	aac	atc	ggt	ggc	643	
Gly	Ile	Ser	His	Tyr	Gly	Asn	Cys	Leu	Gly	Leu	Pro	Asn	Ile	Gly	Gly		
			170					175						180			
gaa	acc	gtc	ttc	gac	gat	tcc	tac	gca	ggt	aac	cca	ctg	gtc	aac	gca	691	
Glu	Thr	Val	Phe	Asp	Asp	Ser	Tyr	Ala	Gly	Asn	Pro	Leu	Val	Asn	Ala		
			185					190					195				
ctg	tgc	gtg	ggt	acc	ctc	aag	gtg	gaa	gac	ctc	aag	ctt	gca	ttc	gca	739	
Leu	Cys	Val	Gly	Thr	Leu	Lys	Val	Glu	Asp	Leu	Lys	Leu	Ala	Phe	Ala		
		200					205					210					
tcc	ggc	acc	ggc	aac	aag	gtg	atc	ctg	ttc	ggt	tcc	cgc	acc	ggc	ctt	787	
Ser	Gly	Thr	Gly	Asn	Lys	Val	Ile	Leu	Phe	Gly	Ser	Arg	Thr	Gly	Leu		
	215					220					225						
gat	ggc	atc	ggt	ggc	gtg	tcc	gtc	ctg	ggt	tcc	gca	tcc	ttc	gaa	gaa	835	
Asp	Gly	Ile	Gly	Gly	Val	Ser	Val	Leu	Gly	Ser	Ala	Ser	Phe	Glu	Glu		
	230				235					240					245		
ggc	gaa	gag	cgc	aag	ctc	cca	gct	gtt	cag	gtt	ggc	gat	cct	ttc	gca	883	
Gly	Glu	Glu	Arg	Lys	Leu	Pro	Ala	Val	Gln	Val	Gly	Asp	Pro	Phe	Ala		
				250					255					260			
gag	aag	gta	ctc	atc	gag	tgc	tgc	ctc	gag	ctg	tac	aag	gct	ggc	gtc	931	
Glu	Lys	Val	Leu	Ile	Glu	Cys	Cys	Leu	Glu	Leu	Tyr	Lys	Ala	Gly	Val		
			265					270					275				
gtg	gtc	ggt	att	cag	gac	ctc	ggt	ggc	ggc	gga	ctt	gcg	tgt	gca	acc	979	
Val	Val	Gly	Ile	Gln	Asp	Leu	Gly	Gly	Gly	Gly	Leu	Ala	Cys	Ala	Thr		
		280					285					290					
tct	gag	ctg	gca	gcc	gca	ggc	gac	ggc	ggc	atg	cgc	gtc	aac	cta	gac	1027	

Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met Arg Val Asn Leu Asp
 295 300 305

aac gtc cca ctg cgc gca gag aac atg tct gca gct gaa atc ctg gct
 1075

Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala Ala Glu Ile Leu Ala
 310 315 320 325

tcc gag tcc cag gag cgc atg tgt gct gtt gtc acc cct gaa aac gtt
 1123

Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val Thr Pro Glu Asn Val
 330 335 340

gag cgt ttc ctc gag atc tgt gca aag tgg gat gtc acc tgc gca gaa
 1171

Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp Val Thr Cys Ala Glu
 345 350 355

atc ggc gaa gtt acc gac gag aag gac cgc tac gtt gtg gtc cac aac
 1219

Ile Gly Glu Val Thr Asp Glu Lys Asp Arg Tyr Val Val Val His Asn
 360 365 370

ggt gaa gtt gtt atc gac gca cct cca tca acc atc gat gaa ggc cct
 1267

Gly Glu Val Val Ile Asp Ala Pro Pro Ser Thr Ile Asp Glu Gly Pro
 375 380 385

gtc tac aac cgc cca gtt gct cgc cct gag aac cag gac gaa ctg cag
 1315

Val Tyr Asn Arg Pro Val Ala Arg Pro Glu Asn Gln Asp Glu Leu Gln
 390 395 400 405

ctc gaa ggc gag atc gct cgc cca gtc gac gtt gaa gag atc aag gct
 1363

Leu Glu Gly Glu Ile Ala Arg Pro Val Asp Val Glu Glu Ile Lys Ala
 410 415 420

gct tgg ctg aag ctt gtc gct tca cca gca ctt gca tcc cgc gcg ttt
 1411

Ala Trp Leu Lys Leu Val Ala Ser Pro Ala Leu Ala Ser Arg Ala Phe
 425 430 435

atc acc gag cag tac gac cgc tac gtc cgc ggc aac acc gtt cag gca
 1459

Ile Thr Glu Gln Tyr Asp Arg Tyr Val Arg Gly Asn Thr Val Gln Ala
 440 445 450

aag aac gcc aat gct ggc gtc ttg cgt atc gac gaa gag acc aac cgt
 1507

Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp Glu Glu Thr Asn Arg
 455 460 465

ggc gtt gcg atc tcc gcc gac gca tcc ggc cgt tac acc aag ctc gag
 1555

Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys Leu Glu
 470 475 480 485

cca aac act ggc gcg cag ctt gca ctg gct gag gct tac cgc aac gtg
 1603

Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg Asn Val

490	495	500
gtc tcc acc ggt gca cgc cca gtg gct gtc acc aac tgc ctg aac ttc		
1651		
Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr Asn Cys Leu Asn Phe		
505	510	515
ggg tcc cca gaa aac gct ggt gtt atg tgg cag ttc aag gaa gca gtc		
1699		
Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln Phe Lys Glu Ala Val		
520	525	530
cac ggt ctg gca gac gga tcc aag ctt ttg ggc att cca gtg tcc ggc		
1747		
His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly Ile Pro Val Ser Gly		
535	540	545
ggg aac gtc tcc ttc tac aac cag act ggt gac gag ccc atc ctg cca		
1795		
Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp Glu Pro Ile Leu Pro		
550	555	560
acc cca gtc gtg ggt gtt ttg gga gtc ttg gac aac gtc gag cag agc		
1843		
Thr Pro Val Val Gly Val Leu Gly Val Leu Asp Asn Val Glu Gln Ser		
570	575	580
atc ggc aac gtc ctc cca tcc gag gac aac gat ctc tac ctc ctg ggt		
1891		
Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp Leu Tyr Leu Leu Gly		
585	590	595
gag acc ttc gat gag ttc ggt ggc tcc atc tgg cag cag gtt tct ggc		
1939		
Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp Gln Gln Val Ser Gly		
600	605	610
gct ggc ctc aac ggt ctg cca cca gta gtt gac ctg ctc aac gag cag		
1987		
Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp Leu Leu Asn Glu Gln		
615	620	625
cgt ctt gca gac ctg ttc gtc ggt tct gat ctg ttt gct gca tcc cac		
2035		
Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu Phe Ala Ala Ser His		
630	635	640
gat ctg tct gag ggc ggc ctt ggc cag acc ctc gca gag ctt gcg atc		
2083		
Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu Ala Glu Leu Ala Ile		
650	655	660
cac cag aaa aag gga atg gat gtt gat ctc tcc cag atc cac cca tcc		
2131		
His Gln Lys Lys Gly Met Asp Val Asp Leu Ser Gln Ile His Pro Ser		
665	670	675
ctg ttc acc tca ctg ttt gct gag tcc gct tcc cgc atc gtg gtt gca		
2179		
Leu Phe Thr Ser Leu Phe Ala Glu Ser Ala Ser Arg Ile Val Val Ala		
680	685	690

acc aac cgc ggc gaa gag ttg gaa aag cgc gca gca gag ctg ggt gtt
2227

Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala Ala Glu Leu Gly Val
695 700 705

cca gtg ttc aag ctg ggc tgc acc aac gat tca gcc gtc atc gct gtc
2275

Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser Ala Val Ile Ala Val
710 715 720 725

aag ggc gca gac gtt gag ttc act gtt tcc gtg gag gaa ctc cgc gaa
2323

Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val Glu Glu Leu Arg Glu
730 735 740

gca tgg acc aac act ttg cct gag gcc ttc ggt cac gca gtt gga gct
2371

Ala Trp Thr Asn Thr Leu Pro Glu Ala Phe Gly His Ala Val Gly Ala
745 750 755

aac gca gta gtt gca taattttctg ctgtgaagcc ggg
2409

Asn Ala Val Val Ala
760

<210> 912

<211> 762

<212> PRT

<213> Corynebacterium glutamicum

<400> 912

Met Ser Thr Phe Val Asn Asp Thr Val Glu Asp Ala Ile Lys Thr Pro
1 5 10 15

Glu Leu Asp Gln Pro Phe Glu Ala Leu Gly Leu Lys Asp Asp Glu Tyr
20 25 30

Ala Arg Ile Lys Glu Ile Leu Gly Arg Arg Pro Thr Asp Ala Glu Leu
35 40 45

Thr Val Tyr Ser Val Met Trp Ser Glu His Cys Ser Tyr Lys Ser Ser
50 55 60

Lys Val His Leu Arg Tyr Phe Gly Glu Thr Thr Thr Glu Glu Met Ala
65 70 75 80

Ser Lys Ile Leu Ala Gly Ile Gly Glu Asn Ala Gly Val Val Asp Ile
85 90 95

Gly Asp Gly Asn Ala Val Thr Phe Arg Val Glu Ser His Asn His Pro
100 105 110

Ser Phe Val Glu Pro His Gln Gly Ala Ala Thr Gly Val Gly Gly Ile
115 120 125

Val Arg Asp Ile Met Ala Met Gly Ala Arg Pro Ile Ala Val Met Asp
130 135 140

Gln Leu Arg Phe Gly Ala Leu Asp Asn Pro Asp Thr Gln Arg Val Phe

145	150	155	160
Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu	165	170	175
Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn	180	185	190
Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu	195	200	205
Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly	210	215	220
Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser	225	230	235
Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val	245	250	255
Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu	260	265	270
Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly	275	280	285
Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met	290	295	300
Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala	305	310	315
Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val	325	330	335
Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp	340	345	350
Val Thr Cys Ala Glu Ile Gly Glu Val Thr Asp Glu Lys Asp Arg Tyr	355	360	365
Val Val Val His Asn Gly Glu Val Val Ile Asp Ala Pro Pro Ser Thr	370	375	380
Ile Asp Glu Gly Pro Val Tyr Asn Arg Pro Val Ala Arg Pro Glu Asn	385	390	395
Gln Asp Glu Leu Gln Leu Glu Gly Glu Ile Ala Arg Pro Val Asp Val	405	410	415
Glu Glu Ile Lys Ala Ala Trp Leu Lys Leu Val Ala Ser Pro Ala Leu	420	425	430
Ala Ser Arg Ala Phe Ile Thr Glu Gln Tyr Asp Arg Tyr Val Arg Gly	435	440	445
Asn Thr Val Gln Ala Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp	450	455	460
Glu Glu Thr Asn Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg	465	470	475
			480

Tyr Thr Lys Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu
 485 490 495
 Ala Tyr Arg Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr
 500 505 510
 Asn Cys Leu Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln
 515 520 525
 Phe Lys Glu Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly
 530 535 540
 Ile Pro Val Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp
 545 550 555 560
 Glu Pro Ile Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp
 565 570 575
 Asn Val Glu Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp
 580 585 590
 Leu Tyr Leu Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp
 595 600 605
 Gln Gln Val Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp
 610 615 620
 Leu Leu Asn Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu
 625 630 635 640
 Phe Ala Ala Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu
 645 650 655
 Ala Glu Leu Ala Ile His Gln Lys Lys Gly Met Asp Val Asp Leu Ser
 660 665 670
 Gln Ile His Pro Ser Leu Phe Thr Ser Leu Phe Ala Glu Ser Ala Ser
 675 680 685
 Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala
 690 695 700
 Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser
 705 710 715 720
 Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val
 725 730 735
 Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu Ala Phe Gly
 740 745 750
 His Ala Val Gly Ala Asn Ala Val Val Ala
 755 760

<210> 913

<211> 638

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (54) .. (638)

<223> FRXA02805

<400> 913

tgtgatggat cagctgcgtt tcgggtgcac tggacaaccc agacacccag cgtgtg ttt 59
 Val Phe
 1

cct ggc gtt gtt gac ggc att tcc cat tac ggc aac tgc ctc ggc ctg 107
 Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu
 5 10 15

cca aac atc ggt ggc gaa acc gtc ttc gac gat tcc tac gca ggt aac 155
 Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn
 20 25 30

cca ctg gtc aac gca ctg tgc gtg ggt acc ctc aag gtg gaa gac ctc 203
 Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu
 35 40 45 50

aag ctt gca ttc gca tcc ggc acc ggc aac aag gtg atc ctg ttc ggt 251
 Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly
 55 60 65

tcc cgc acc ggc ctt gat ggc atc ggt ggc gtg tcc gtc ctg ggt tcc 299
 Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser
 70 75 80

gca tcc ttc gaa gaa ggc gaa gag cgc aag ctc cca gct gtt cag gtt 347
 Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val
 85 90 95

ggc gat cct ttc gca gag aag gta ctc atc gag tgc tgc ctc gag ctg 395
 Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu
 100 105 110

tac aag gct ggc gtc gtg gtc ggt att cag gac ctc ggt ggc ggc gga 443
 Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly
 115 120 125 130

ctt gcg tgt gca acc tct gag ctg gca gcc gca ggc gac ggc ggc atg 491
 Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met
 135 140 145

cgc gtc aac cta gac aac gtc cca ctg cgc gca gag aac atg tct gca 539
 Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala
 150 155 160

gct gaa atc ctg gct tcc gag tcc cag gag cgc atg tgt gct gtt gtc 587
 Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val
 165 170 175

acc cct gaa aac gtt gag cgt ttc ctc gag atc tgt gca aag tgg gat 635
 Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp
 180 185 190

gtc 638
 Val
 195

<210> 914
 <211> 195
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 914

Val Phe Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu
 1 5 10 15

Gly Leu Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala
 20 25 30

Gly Asn Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu
 35 40 45

Asp Leu Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu
 50 55 60

Phe Gly Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu
 65 70 75 80

Gly Ser Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val
 85 90 95

Gln Val Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu
 100 105 110

Glu Leu Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly
 115 120 125

Gly Gly Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly
 130 135 140

Gly Met Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met
 145 150 155 160

Ser Ala Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala
 165 170 175

Val Val Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys
 180 185 190

Trp Asp Val
 195

<210> 915
 <211> 697
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (23) .. (697)

<223> FRXA00537

<400> 915

caacagcact tgcattccgc gcgtg tat cac cga gca gta ctg aac gct acg 52
 Val Tyr His Arg Ala Val Leu Asn Ala Thr

	1	5	10	
tcc gcg gca aca ccg ttc aag caa aag aac gcc aat gct ggc gtc ttg				100
Ser Ala Ala Thr Pro Phe Lys Gln Lys Asn Ala Asn Ala Gly Val Leu				
	15	20	25	
cgt atc gac gaa gag acc anc cgt ggc gtt gcg atc tcc gcc gac gca				148
Arg Ile Asp Glu Glu Thr Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala				
	30	35	40	
tcc ggc cgt tac acc aag ctc gag cca aac act ggc gcg cag ctt gca				196
Ser Gly Arg Tyr Thr Lys Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala				
	45	50	55	
ctg gct gag gct tac cgc aac gtg gtc tcc acc ggt gca cgc cca gtg				244
Leu Ala Glu Ala Tyr Arg Asn Val Val Ser Thr Gly Ala Arg Pro Val				
	60	65	70	
gct gtc acc aac tgc ctg aac ttc ggt tcc cca gaa aac gct ggt gtt				292
Ala Val Thr Asn Cys Leu Asn Phe Gly Ser Pro Glu Asn Ala Gly Val				
	75	80	85	90
atg tgg cag ttc aag gaa gca gtc cac ggt ctg gca gac gga tcc aag				340
Met Trp Gln Phe Lys Glu Ala Val His Gly Leu Ala Asp Gly Ser Lys				
	95	100	105	
ctt ttg ggc att cca gtg tcc ggc ggt aac gtc tcc ttc tac aac cag				388
Leu Leu Gly Ile Pro Val Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln				
	110	115	120	
act ggt gac gag ccc atc ctg cca acc cca gtc gtg ggt gtt ttg gga				436
Thr Gly Asp Glu Pro Ile Leu Pro Thr Pro Val Val Gly Val Leu Gly				
	125	130	135	
gtc ttg gac aac gtc gag cag agc atc ggc aac gtc ctc cca tcc gag				484
Val Leu Asp Asn Val Glu Gln Ser Ile Gly Asn Val Leu Pro Ser Glu				
	140	145	150	
gac aac gat ctc tac ctc ctg ggt gag acc ttc gat gag ttc ggt ggc				532
Asp Asn Asp Leu Tyr Leu Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly				
	155	160	165	170
tcc atc tgg cag cag gtt tct ggc gct ggc ctc aac ggt ctg cca cca				580
Ser Ile Trp Gln Gln Val Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro				
	175	180	185	
gta gtt gac ctg ctc aac gag cag cgt ctt gca gac ctg ttc gtc ggt				628
Val Val Asp Leu Leu Asn Glu Gln Arg Leu Ala Asp Leu Phe Val Gly				
	190	195	200	
tct gat ctg ttt gct gca tcc cac gat ctg tct gag ggc ggc ctt ggc				676
Ser Asp Leu Phe Ala Ala Ser His Asp Leu Ser Glu Gly Gly Leu Gly				
	205	210	215	
cag acc ctc gca gag ctt gcg				697
Gln Thr Leu Ala Glu Leu Ala				
	220	225		

<210> 916

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 916

Val Tyr His Arg Ala Val Leu Asn Ala Thr Ser Ala Ala Thr Pro Phe
 1 5 10 15

Lys Gln Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp Glu Glu Thr
 20 25 30

Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys
 35 40 45

Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg
 50 55 60

Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr Asn Cys Leu
 65 70 75 80

Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln Phe Lys Glu
 85 90 95

Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly Ile Pro Val
 100 105 110

Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp Glu Pro Ile
 115 120 125

Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp Asn Val Glu
 130 135 140

Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp Leu Tyr Leu
 145 150 155 160

Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp Gln Gln Val
 165 170 175

Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp Leu Leu Asn
 180 185 190

Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu Phe Ala Ala
 195 200 205

Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu Ala Glu Leu
 210 215 220

Ala
 225

<210> 917

<211> 302

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) .. (279)

<223> FRXA00561

<400> 917

```

ctc ttc cca gat cca ccc atc cct gtt cac ctc act tgt ttg ctg agt      48
Leu Phe Pro Asp Pro Pro Ile Pro Val His Leu Thr Cys Leu Leu Ser
  1               5               10               15

ccc gct tcc cgc atc gtg gtt gca acc aac cgc ggc gaa gag ttg gaa      96
Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu
              20               25               30

aag cgc gca gca gag ctg ggt gtt cca gtg ttc aag ctg ggc tgc acc      144
Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr
              35               40               45

aac gat tca gcc gtc atc gct gtc aag ggc gca gac gtt gag ttc act      192
Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr
              50               55               60

gtt tcc gtg gag gaa ctc cgc gaa gca tgg acc aac act ttg cct gag      240
Val Ser Val Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu
  65               70               75               80

gcc ttc ggt cac gca gtt gga gct aac gca gta gtt gca taattttctg      289
Ala Phe Gly His Ala Val Gly Ala Asn Ala Val Val Ala
              85               90

ctgtgaagcc ggg                                                    302

```

<210> 918

<211> 93

<212> PRT

<213> Corynebacterium glutamicum

<400> 918

```

Leu Phe Pro Asp Pro Pro Ile Pro Val His Leu Thr Cys Leu Leu Ser
  1               5               10               15

Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu
              20               25               30

Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr
              35               40               45

Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr
              50               55               60

Val Ser Val Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu
  65               70               75               80

Ala Phe Gly His Ala Val Gly Ala Asn Ala Val Val Ala
              85               90

```

<210> 919

<211> 792

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(769)

<223> RXA00541

<400> 919

```

atgattccgt caccgaagct gacctaaaga aaattgctga aaccctcctc gcaaacaccg 60

tcacgaaga cttcgatgtg gtgggagttg aggtcgcgaa gtg agc gcc aaa atc 115
                               Val Ser Ala Lys Ile
                               1 5

ggt gtc att acc ttc cca ggc acc ctt gac gat gta gat gca gca cgc 163
Gly Val Ile Thr Phe Pro Gly Thr Leu Asp Asp Val Asp Ala Ala Arg
                               10 15 20

gct gct cgc atc gca ggt gca gaa gta atc agc ctg tgg cac gct gac 211
Ala Ala Arg Ile Ala Gly Ala Glu Val Ile Ser Leu Trp His Ala Asp
                               25 30 35

gag gat ctc aag ggc gtc gac gca gtt gtc gtt ccc ggt gga ttc tcc 259
Glu Asp Leu Lys Gly Val Asp Ala Val Val Val Pro Gly Gly Phe Ser
                               40 45 50

tac ggc gat tac ctg cgc acc ggt gca atc tct gca ctg gcg cca gta 307
Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser Ala Leu Ala Pro Val
                               55 60 65

atg cag tcc gtg att gag cag gcc ggt aag ggt atg cca gtc ttg ggc 355
Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly Met Pro Val Leu Gly
                               70 75 80 85

att tgc aac ggc ttc cag atc ctc acc gaa gca cgc ctg ctt cca ggc 403
Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala Arg Leu Leu Pro Gly
                               90 95 100

gcg ctg acc cgc aac aag ggt ctg cac ttt cac tgt gta gac gca cac 451
Ala Leu Thr Arg Asn Lys Gly Leu His Phe His Cys Val Asp Ala His
                               105 110 115

ctc gtt gta gag aac aac acc act gca tgg acc aac act ttg gaa aag 499
Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr Asn Thr Leu Glu Lys
                               120 125 130

ggt cag cag atc ctt att cct gca aag cac ggt gaa ggt cgc ttc cag 547
Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly Glu Gly Arg Phe Gln
                               135 140 145

gca gac gca gag acc atc gcc cag ctt gag ggt gaa ggc cgc gtg gtg 595
Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly Glu Gly Arg Val Val
                               150 155 160 165

ttc cgt tac acc gat aac ttc aac ggt tcc gtc aac gat atc gcc ggt 643
Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val Asn Asp Ile Ala Gly
                               170 175 180

atc act aat gaa act ggt cgc atc gtc ggt ctc atg ccg cac ccg gaa 691
Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu Met Pro His Pro Glu
                               185 190 195

cat gcc gtc gaa aag cta acc ggc cca tct att gat ggc ctg gag ctg 739
His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile Asp Gly Leu Glu Leu
                               200 205 210

ttc ctg tcc gcc gtt ggc acc atc gcg gct taagaggagt aaatatgagc 789

```

Phe Leu Ser Ala Val Gly Thr Ile Ala Ala
215 220

act

792

<210> 920

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 920

Val Ser Ala Lys Ile Gly Val Ile Thr Phe Pro Gly Thr Leu Asp Asp
1 5 10 15

Val Asp Ala Ala Arg Ala Ala Arg Ile Ala Gly Ala Glu Val Ile Ser
20 25 30

Leu Trp His Ala Asp Glu Asp Leu Lys Gly Val Asp Ala Val Val Val
35 40 45

Pro Gly Gly Phe Ser Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser
50 55 60

Ala Leu Ala Pro Val Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly
65 70 75 80

Met Pro Val Leu Gly Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala
85 90 95

Arg Leu Leu Pro Gly Ala Leu Thr Arg Asn Lys Gly Leu His Phe His
100 105 110

Cys Val Asp Ala His Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr
115 120 125

Asn Thr Leu Glu Lys Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly
130 135 140

Glu Gly Arg Phe Gln Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly
145 150 155 160

Glu Gly Arg Val Val Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val
165 170 175

Asn Asp Ile Ala Gly Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu
180 185 190

Met Pro His Pro Glu His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile
195 200 205

Asp Gly Leu Glu Leu Phe Leu Ser Ala Val Gly Thr Ile Ala Ala
210 215 220

<210> 921

<211> 1014

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(991)

<223> RXA00620

<400> 921

ggatgatccat gtcaggaagc cagcgggtgaa accgggcagtg aaaccagcgg tgaatgctaa 60

aattttccga acacacccga ggggtctaga cttgcctaac atg cgt cct gaa ctc 115
 Met Arg Pro Glu Leu
 1 5

tcc cag tac aag cac ctg tcg gca ggc aag gtc cgt gag atc tac gag 163
 Ser Gln Tyr Lys His Leu Ser Ala Gly Lys Val Arg Glu Ile Tyr Glu
 10 15 20

atc gac gac aag cac atc ctc atg gtg gct tcc gat cgt atc tct gca 211
 Ile Asp Asp Lys His Ile Leu Met Val Ala Ser Asp Arg Ile Ser Ala
 25 30 35

tac gat ttc atc ctc gat acc gaa att cca gac aag ggt cga gtg ctc 259
 Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp Lys Gly Arg Val Leu
 40 45 50

act gcg atg agc cag ttc ttc ttc gac acc atc gat ttt cct aat cac 307
 Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile Asp Phe Pro Asn His
 55 60 65

ctt gca ggt ccc gct gat gat cca cgt atc cca gaa gaa gtt ttg gga 355
 Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro Glu Glu Val Leu Gly
 70 75 80 85

cga gca atg gtg tgc aag aag ctc aac atg ctt cct ttt gaa tgc gtg 403
 Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu Pro Phe Glu Cys Val
 90 95 100

gtt cgt gga tac ctc act ggc tct gga ctt gtt gaa tac aag cag acc 451
 Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val Glu Tyr Lys Gln Thr
 105 110 115

agc tcc gtg tgt gga gtt gag ctc cca gaa ggc ctc gtt gaa tct tct 499
 Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly Leu Val Glu Ser Ser
 120 125 130

cag ctg cct gag cca atc ttt acc cca gcc acc aag gct gac atc ggc 547
 Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr Lys Ala Asp Ile Gly
 135 140 145

gac cac gac atc aat gtc tcc ttt gac gtt gtt gaa gaa cgt ctc ggc 595
 Asp His Asp Ile Asn Val Ser Phe Asp Val Val Glu Glu Arg Leu Gly
 150 155 160 165

gaa gct cgt gcg aac cag ttg cgc gat gcc tct att gct att tac aag 643
 Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser Ile Ala Ile Tyr Lys
 170 175 180

gct gct gct gag atc gcc cgt gac cgt ggc gtc atc ctt gcc gac acc 691
 Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val Ile Leu Ala Asp Thr
 185 190 195

aaa ttt gag ttc ggc atc gat gaa gat ggc acc ctc gtg ctt ggt gat 739
 Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr Leu Val Leu Gly Asp

200	205	210	
gaa gtc ctt acc cca gat tcc tcc cgc tac tgg cct ttg gaa ggc tat			787
Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp Pro Leu Glu Gly Tyr			
215	220	225	
gaa gca gga tct gtg caa cca agc ttt gat aag caa ttc gtg cgc aac			835
Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys Gln Phe Val Arg Asn			
230	235	240	245
tgg ctc acc ggc cct aaa tct ggc tgg gac aag gat tcc ggc ttg gag			883
Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys Asp Ser Gly Leu Glu			
250	255	260	
cca cca gct ctg cca ggt tcc gtt gtt gag gca acc cgc gag cgc tac			931
Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala Thr Arg Glu Arg Tyr			
265	270	275	
atc gag gcc tac gag ctg att tct ggt cag aag ttc tgc cag tgg att			979
Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys Phe Cys Gln Trp Ile			
280	285	290	
ggt tct tgc gtc taagctgctt gattttccct aaa			
1014			
Gly Ser Cys Val			
295			

<210> 922

<211> 297

<212> PRT

<213> Corynebacterium glutamicum

<400> 922

Met	Arg	Pro	Glu	Leu	Ser	Gln	Tyr	Lys	His	Leu	Ser	Ala	Gly	Lys	Val
1				5					10					15	

Arg	Glu	Ile	Tyr	Glu	Ile	Asp	Asp	Lys	His	Ile	Leu	Met	Val	Ala	Ser
			20					25					30		

Asp	Arg	Ile	Ser	Ala	Tyr	Asp	Phe	Ile	Leu	Asp	Thr	Glu	Ile	Pro	Asp
			35				40					45			

Lys	Gly	Arg	Val	Leu	Thr	Ala	Met	Ser	Gln	Phe	Phe	Phe	Asp	Thr	Ile
	50					55					60				

Asp	Phe	Pro	Asn	His	Leu	Ala	Gly	Pro	Ala	Asp	Asp	Pro	Arg	Ile	Pro
65					70					75				80	

Glu	Glu	Val	Leu	Gly	Arg	Ala	Met	Val	Cys	Lys	Lys	Leu	Asn	Met	Leu
			85					90					95		

Pro	Phe	Glu	Cys	Val	Val	Arg	Gly	Tyr	Leu	Thr	Gly	Ser	Gly	Leu	Val
			100				105					110			

Glu	Tyr	Lys	Gln	Thr	Ser	Ser	Val	Cys	Gly	Val	Glu	Leu	Pro	Glu	Gly
		115					120					125			

Leu	Val	Glu	Ser	Ser	Gln	Leu	Pro	Glu	Pro	Ile	Phe	Thr	Pro	Ala	Thr
		130				135					140				

Lys Ala Asp Ile Gly Asp His Asp Ile Asn Val Ser Phe Asp Val Val
 145 150 155 160
 Glu Glu Arg Leu Gly Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser
 165 170 175
 Ile Ala Ile Tyr Lys Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val
 180 185 190
 Ile Leu Ala Asp Thr Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr
 195 200 205
 Leu Val Leu Gly Asp Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp
 210 215 220
 Pro Leu Glu Gly Tyr Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys
 225 230 235 240
 Gln Phe Val Arg Asn Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys
 245 250 255
 Asp Ser Gly Leu Glu Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala
 260 265 270
 Thr Arg Glu Arg Tyr Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys
 275 280 285
 Phe Cys Gln Trp Ile Gly Ser Cys Val
 290 295

<210> 923

<211> 1293

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1270)

<223> RXN00770

<400> 923

~~ccatgggtct gccacagga aacagcaacg cagacctaag ccacaagatg caagcaaccg 60~~

cctcaagtta agatcggtag gcgatagggg ttgagcattt ttg ctc tcc ccg tat 115
 Leu Leu Ser Pro Tyr
 1 5
 gcg tgg ggg ttg tcc cgc gca ctt tta gac agt tat gtt cct aat aag 163
 Ala Trp Gly Leu Ser Arg Ala Leu Leu Asp Ser Tyr Val Pro Asn Lys
 10 15 20
 ttc caa acc cca gca gga gaa gcg aag tac acg atg agt gat cac cag 211
 Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr Met Ser Asp His Gln
 25 30 35
 gac acc acc gcc gaa ggc gtt tca tac gca gca gca gga gtc gac atc 259
 Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala Ala Gly Val Asp Ile
 40 45 50
 gaa gcc ggc gat cgt gcc gtc gaa ctc ttt gca cca atg gcc aag cgc 307

Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala Pro Met Ala Lys Arg
 55 60 65

gcc acc cgc cca gag gtt ctt ggc aac ctc gga ggc ttc gca gga ctc 355
 Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly Gly Phe Ala Gly Leu
 70 75 80 85

ttt gag ctc gga aaa tac aag aag cca atc ctc gca gca gga tct gac 403
 Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu Ala Ala Gly Ser Asp
 90 95 100

gga gtc ggc acc aag ctt gtc atc gcc cag atg atg gac aag cac gac 451
 Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met Met Asp Lys His Asp
 105 110 115

acc atc ggc atc gac ctt gtt gca atg tgt gtg gat gac ctc gtt gtc 499
 Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val Asp Asp Leu Val Val
 120 125 130

acc ggc gca gag cca ctg ttc ctc cag gac tac atc gcc atc ggc aag 547
 Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr Ile Ala Ile Gly Lys
 135 140 145

gtt gtc cca gag cac gtt gct gag atc gtc tcc ggt atc gca gaa ggc 595
 Val Val Pro Glu His Val Ala Glu Ile Val Ser Gly Ile Ala Glu Gly
 150 155 160 165

tgt gtc cag gca ggc tgt gct ctg ctc ggt ggc gaa acc gca gaa cac 643
 Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly Glu Thr Ala Glu His
 170 175 180

cca ggt gtt atg gaa cca gac cac tac gat gtc tcc gca act gca gtc 691
 Pro Gly Val Met Glu Pro Asp His Tyr Asp Val Ser Ala Thr Ala Val
 185 190 195

ggc gtt gtc gaa gca gat gaa ctg cta gga cca gac cgc gtc cgc gca 739
 Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro Asp Arg Val Arg Ala
 200 205 210

ggc gac ctc atc ggc atg gct tcc tcc ggt ctg cac tcc aac ggt 787
 Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly Leu His Ser Asn Gly
 215 220 225

tac tcc ctg gct cgc cac gtc ctc ctg gaa aag gca ggc ctg gcg ctt 835
 Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys Ala Gly Leu Ala Leu
 230 235 240 245

gac gga cac atc gaa gaa ctc gga cgc acc ctc ggt gaa gaa ctt ctc 883
 Asp Gly His Ile Glu Glu Leu Gly Arg Thr Leu Gly Glu Glu Leu Leu
 250 255 260

gag cca acc cgc atc tac gcc aag gac tgc ctg gca ctg atc gca gag 931
 Glu Pro Thr Arg Ile Tyr Ala Lys Asp Cys Leu Ala Leu Ile Ala Glu
 265 270 275

tgc gaa gtt cac acc ttc tgc cac gtc acc ggc ggc ggc ctc gca ggc 979
 Cys Glu Val His Thr Phe Cys His Val Thr Gly Gly Gly Leu Ala Gly
 280 285 290

aac ctc gag cgg gtt gtc cca gaa ggg ctc gtc gca gaa atg tcc cga
 1027

Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val Ala Glu Met Ser Arg
 295 300 305

gca act tgg acc cca ggc caa atc ttc cgc acc atc tcc tct gtg ggc
 1075

Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr Ile Ser Ser Val Gly
 310 315 320 325

aag gtt tcc cgc gaa gaa atg gaa aag acc ttc aac atg ggt gtc ggc
 1123

Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe Asn Met Gly Val Gly
 330 335 340

atg gtt gca gtc gtt gct gaa aag gac cgc gac cgc gcc ctg gca atg
 1171

Met Val Ala Val Val Ala Glu Lys Asp Arg Asp Arg Ala Leu Ala Met
 345 350 355

ctc acc gca cgt cac att gac tgc tgg gaa atc gga acc gta cgc aac
 1219

Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile Gly Thr Val Arg Asn
 360 365 370

ggt gaa gag gga gag cct cgc gtg atc ctc aac ggc gag cac cct ggc
 1267

Gly Glu Glu Gly Glu Pro Arg Val Ile Leu Asn Gly Glu His Pro Gly
 375 380 385

tac taagcccaac tgtctgctct aag

1293

Tyr

390

<210> 924

<211> 390

<212> PRT

<213> Corynebacterium glutamicum

<400> 924

Leu Leu Ser Pro Tyr Ala Trp Gly Leu Ser Arg Ala Leu Leu Asp Ser
 1 5 10 15

Tyr Val Pro Asn Lys Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr
 20 25 30

Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala
 35 40 45

Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala
 50 55 60

Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly
 65 70 75 80

Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu
 85 90 95

Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met
 100 105 110

Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val
 115 120 125

Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr
 130 135 140

Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser
 145 150 155 160

Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly
 165 170 175

Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val
 180 185 190

Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro
 195 200 205

Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly
 210 215 220

Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys
 225 230 235 240

Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Leu
 245 250 255

Gly Glu Glu Leu Leu Glu Pro Thr Arg Ile Tyr Ala Lys Asp Cys Leu
 260 265 270

Ala Leu Ile Ala Glu Cys Glu Val His Thr Phe Cys His Val Thr Gly
 275 280 285

Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val
 290 295 300

Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr
 305 310 315 320

Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe
 325 330 335

Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys Asp Arg Asp
 340 345 350

Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile
 355 360 365

Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val Ile Leu Asn
 370 375 380

Gly Glu His Pro Gly Tyr
 385 390

<210> 925

<211> 818

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (15)..(818)

<223> FRXA00557

<400> 925

tgggttgagc atttttg ctc tcc ccg tat gcg tgg ggg ttg tcc cgc gca	50
Leu Leu Ser Pro Tyr Ala Trp Gly Leu Ser Arg Ala	
1 5 10	
ctt tta gac agt tat gtt cct aat aag ttc caa acc cca gca gga gaa	98
Leu Leu Asp Ser Tyr Val Pro Asn Lys Phe Gln Thr Pro Ala Gly Glu	
15 20 25	
gcg aag tac acg atg agt gat cac cag gac acc acc gcc gaa ggc gtt	146
Ala Lys Tyr Thr Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val	
30 35 40	
tca tac gca gca gca gga gtc gac atc gaa gcc ggc gat cgt gcc gtc	194
Ser Tyr Ala Ala Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val	
45 50 55 60	
gaa ctc ttt gca cca atg gcc aag cgc gcc acc cgc cca gag gtt ctt	242
Glu Leu Phe Ala Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu	
65 70 75	
ggc aac ctc gga ggc ttc gca gga ctc ttt gag ctc gga aaa tac aag	290
Gly Asn Leu Gly Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys	
80 85 90	
aag cca atc ctc gca gca gga tct gac gga gtc ggc acc aag ctt gtc	338
Lys Pro Ile Leu Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val	
95 100 105	
atc gcc cag atg atg gac aag cac gac acc atc ggc atc gac ctt gtt	386
Ile Ala Gln Met Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val	
110 115 120	
gca atg tgt gtg gat gac ctc gtt gtc acc ggc gca gag cca ctg ttc	434
Ala Met Cys Val Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe	
125 130 135 140	
ctc cag gac tac atc gcc atc ggc aag gtt gtc cca gag cac gtt gct	482
Leu Gln Asp Tyr Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala	
145 150 155	
gag atc gtc tcc ggt atc gca gaa ggc tgt gtc cag gca ggc tgt gct	530
Glu Ile Val Ser Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala	
160 165 170	
ctg ctc ggt ggc gaa acc gca gaa cac cca ggt gtt atg gaa cca gac	578
Leu Leu Gly Gly Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp	
175 180 185	
cac tac gat gtc tcc gca act gca gtc ggc gtt gtc gaa gca gat gaa	626
His Tyr Asp Val Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu	
190 195 200	
ctg cta gga cca gac cgc gtc cgc gca ggc gac gtc ctc atc ggc atg	674
Leu Leu Gly Pro Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met	
205 210 215 220	

gct tcc tcc ggt ctg cac tcc aac ggt tac tcc ctg gct cgc cac gtc 722
 Ala Ser Ser Gly Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val
 225 230 235

ctc ctg gaa aag gca ggc ctg gcg ctt gac gga cac atc gaa gaa ctc 770
 Leu Leu Glu Lys Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu
 240 245 250

gga cgc acc ccc ggt gaa gaa ctt ctc gag cca acc cgc atg tac gcc 818
 Gly Arg Thr Pro Gly Glu Glu Leu Leu Glu Pro Thr Arg Met Tyr Ala
 255 260 265

<210> 926

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 926

Leu Leu Ser Pro Tyr Ala Trp Gly Leu Ser Arg Ala Leu Leu Asp Ser
 1 5 10 15

Tyr Val Pro Asn Lys Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr
 20 25 30

Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala
 35 40 45

Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala
 50 55 60

Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly
 65 70 75 80

Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu
 85 90 95

Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met
 100 105 110

Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val
 115 120 125

Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr
 130 135 140

Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser
 145 150 155 160

Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly
 165 170 175

Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val
 180 185 190

Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro
 195 200 205

Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly
 210 215 220

Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys
 225 230 235 240

Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Pro
 245 250 255

Gly Glu Glu Leu Leu Glu Pro Thr Arg Met Tyr Ala
 260 265

<210> 927

<211> 338

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(315)

<223> FRXA00770

<400> 927

gtc acc ggc ggc ggc ctc gca ggc aac ctc gag cgg gtt gtc cca gaa 48
 Val Thr Gly Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu
 1 5 10 15

ggg ctc gtc gca gaa atg tcc cga gca act tgg acc cca ggc caa atc 96
 Gly Leu Val Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile
 20 25 30

ttc cgc acc atc tcc tct gtg ggc aag gtt tcc cgc gaa gaa atg gaa 144
 Phe Arg Thr Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu
 35 40 45

aag acc ttc aac atg ggt gtc ggc atg gtt gca gtc gtt gct gaa aag 192
 Lys Thr Phe Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys
 50 55 60

gac cgc gac cgc gcc ctg gca atg ctc acc gca cgt cac att gac tgc 240
 Asp Arg Asp Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys
 65 70 75 80

tgg gaa atc gga acc gta cgc aac ggt gaa gag gga gag cct cgc gtg 288
 Trp Glu Ile Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val
 85 90 95

atc ctc aac ggc gag cac cct ggc tac taagcccaac tgtctgtctct 335
 Ile Leu Asn Gly Glu His Pro Gly Tyr
 100 105

aag 338

<210> 928

<211> 105

<212> PRT

<213> Corynebacterium glutamicum

<400> 928

Val Thr Gly Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu
 1 5 10 15

<400> 929																
accaccgacc	ctatgtaatc	aaccagggttc	ccaaggctcg	aaaagtggaa	gcgctgctca	60										
aagatcttac	attttggtga	aggcgttata	gttaggactt	gtg	act	tct	aca	gga	115							
				Val	Thr	Ser	Thr	Gly								
				1				5								
aac	caa	gcc	cac	gct	cca	gga	atg	ccc	atc	gtc	gca	gta	att	ggg	gac	163
Asn	Gln	Ala	His	Ala	Pro	Gly	Met	Pro	Ile	Val	Ala	Val	Ile	Gly	Asp	
				10				15						20		
ggc	caa	tta	gcc	cgc	atg	atg	cag	acc	tcc	gcc	atc	gaa	ctc	gga	caa	211
Gly	Gln	Leu	Ala	Arg	Met	Met	Gln	Thr	Ser	Ala	Ile	Glu	Leu	Gly	Gln	
			25					30						35		
tca	ctg	cga	gtt	cta	gct	gga	gcg	ccg	gat	tcc	tcc	gca	gct	caa	gta	259
Ser	Leu	Arg	Val	Leu	Ala	Gly	Ala	Pro	Asp	Ser	Ser	Ala	Ala	Gln	Val	
		40					45					50				
gct	gct	gat	gtt	gtt	ctc	ggc	gat	tac	acc	aac	att	gat	gat	ctg	cgc	307
Ala	Ala	Asp	Val	Val	Leu	Gly	Asp	Tyr	Thr	Asn	Ile	Asp	Asp	Leu	Arg	
		55				60					65					
gtc	gcc	atc	gaa	ggc	gcc	gat	gtg	atg	acc	ttc	gac	cac	gag	cac	gtc	355
Val	Ala	Ile	Glu	Gly	Ala	Asp	Val	Met	Thr	Phe	Asp	His	Glu	His	Val	
	70				75					80					85	
ccc	aac	gaa	cac	ctg	cac	caa	ctc	atc	gca	gaa	ggc	gtc	aac	gtt	cag	403
Pro	Asn	Glu	His	Leu	His	Gln	Leu	Ile	Ala	Glu	Gly	Val	Asn	Val	Gln	
				90					95					100		
cca	cgc	cca	qaa	gcg	ctg	gtc	aac	gca	caa	gac	aaa	ctt	gtc	atg	cgc	451

Pro	Arg	Pro	Glu	Ala	Leu	Val	Asn	Ala	Gln	Asp	Lys	Leu	Val	Met	Arg		
			105					110					115				
aag	cgt	cta	cgt	gaa	ctc	ggc	gca	cca	gtc	cca	cca	ttt	gct	gcc	att	499	
Lys	Arg	Leu	Arg	Glu	Leu	Gly	Ala	Pro	Val	Pro	Pro	Phe	Ala	Ala	Ile		
		120					125					130					
gaa	tca	gtc	gaa	gat	gca	gtg	gga	ttc	ttc	gaa	gca	gtt	gat	ggc	caa	547	
Glu	Ser	Val	Glu	Asp	Ala	Val	Gly	Phe	Phe	Glu	Ala	Val	Asp	Gly	Gln		
	135					140					145						
gtt	tgc	ctc	aaa	gca	cgc	cgt	ggc	gga	tac	gac	ggc	aag	ggc	gta	tgg	595	
Val	Cys	Leu	Lys	Ala	Arg	Arg	Gly	Gly	Tyr	Asp	Gly	Lys	Gly	Val	Trp		
150					155					160					165		
ttc	cca	gcc	gat	gta	gca	gag	ctt	cag	tcg	ctt	gtg	gca	gag	ctt	ctc	643	
Phe	Pro	Ala	Asp	Val	Ala	Glu	Leu	Gln	Ser	Leu	Val	Ala	Glu	Leu	Leu		
				170				175						180			
gac	ggc	ggc	acc	cca	ctc	atg	gca	gaa	aag	aaa	gtt	gcc	ctc	aac	agg	691	
Asp	Gly	Gly	Thr	Pro	Leu	Met	Ala	Glu	Lys	Lys	Val	Ala	Leu	Asn	Arg		
			185					190					195				
gaa	ctg	tcc	gcc	atg	gtt	gcc	cgc	acc	cca	agt	gga	gaa	acc	aaa	gcg	739	
Glu	Leu	Ser	Ala	Met	Val	Ala	Arg	Thr	Pro	Ser	Gly	Glu	Thr	Lys	Ala		
	200						205					210					
tgg	cca	gtc	gta	gaa	tca	gtg	cag	aag	aac	ggg	gtg	tgt	gca	gaa	gca	787	
Trp	Pro	Val	Val	Glu	Ser	Val	Gln	Lys	Asn	Gly	Val	Cys	Ala	Glu	Ala		
	215					220					225						
atc	gct	ccc	gca	cct	gaa	cta	tcc	gca	gaa	ctg	cag	gaa	tcc	acc	aga	835	
Ile	Ala	Pro	Ala	Pro	Glu	Leu	Ser	Ala	Glu	Leu	Gln	Glu	Ser	Thr	Arg		
230					235					240				245			
gga	ttg	gcc	cag	aag	atc	gcc	acg	gaa	ctc	ggc	gtc	act	ggg	gtc	ttg	883	
Gly	Leu	Ala	Gln	Lys	Ile	Ala	Thr	Glu	Leu	Gly	Val	Thr	Gly	Val	Leu		
			250					255					260				
gca	gtg	gag	ctt	ttt	gaa	acc	ctc	gac	caa	aac	ggg	cag	cca	gag	atc	931	
Ala	Val	Glu	Leu	Phe	Glu	Thr	Leu	Asp	Gln	Asn	Gly	Gln	Pro	Glu	Ile		
		265					270					275					
ttt	gtc	aac	gag	ctc	gcc	atg	cgt	tca	cac	aac	acc	ggc	cac	tgg	act	979	
Phe	Val	Asn	Glu	Leu	Ala	Met	Arg	Ser	His	Asn	Thr	Gly	His	Trp	Thr		
		280					285					290					
caa	gat	ggc	tgc	gtg	acc	agc	caa	ttc	gag	cag	cac	ctc	cgc	gca	gtc		
1027																	
Gln	Asp	Gly	Cys	Val	Thr	Ser	Gln	Phe	Glu	Gln	His	Leu	Arg	Ala	Val		
	295					300					305						
ctc	gac	tac	cca	ctg	ggg	gct	acc	gac	act	ttg	gct	gat	tac	acc	gtg		
1075																	
Leu	Asp	Tyr	Pro	Leu	Gly	Ala	Thr	Asp	Thr	Leu	Ala	Asp	Tyr	Thr	Val		
310					315					320					325		
atg	gcc	aac	gtg	ctc	ggg	gcc	gac	acc	gac	cca	gag	atg	ccc	atg	gca		
1123																	
Met	Ala	Asn	Val	Leu	Gly	Ala	Asp	Thr	Asp	Pro	Glu	Met	Pro	Met	Ala		
			330					335					340				

acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat gcc aag att cac
1171

Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp Ala Lys Ile His
345 350 355

ctc tac ggc aag gga cat cgc ccg gga cga aag att ggc cac gtc aac
1219

Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile Gly His Val Asn
360 365 370

atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa gcc ctg gcc tgc
1267

Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu Ala Leu Ala Cys
375 380 385

gca tac ttc ctt gtc aac gct cgc tgg gat taggtctttt ctgagcgcta
1317

Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
390 395

gca
1320

<210> 930

<211> 399

<212> PRT

<213> Corynebacterium glutamicum

<400> 930

Val Thr Ser Thr Gly Asn Gln Ala His Ala Pro Gly Met Pro Ile Val
1 5 10 15

Ala Val Ile Gly Asp Gly Gln Leu Ala Arg Met Met Gln Thr Ser Ala
20 25 30

Ile Glu Leu Gly Gln Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser
35 40 45

Ser Ala Ala Gln Val Ala Ala Asp Val Val Leu Gly Asp Tyr Thr Asn
50 55 60

Ile Asp Asp Leu Arg Val Ala Ile Glu Gly Ala Asp Val Met Thr Phe
65 70 75 80

Asp His Glu His Val Pro Asn Glu His Leu His Gln Leu Ile Ala Glu
85 90 95

Gly Val Asn Val Gln Pro Arg Pro Glu Ala Leu Val Asn Ala Gln Asp
100 105 110

Lys Leu Val Met Arg Lys Arg Leu Arg Glu Leu Gly Ala Pro Val Pro
115 120 125

Pro Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu
130 135 140

Ala Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp
145 150 155 160

Gly Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu
 165 170 175
 Val Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys
 180 185 190
 Val Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser
 195 200 205
 Gly Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly
 210 215 220
 Val Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu
 225 230 235 240
 Gln Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly
 245 250 255
 Val Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn
 260 265 270
 Gly Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn
 275 280 285
 Thr Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln
 290 295 300
 His Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu
 305 310 315 320
 Ala Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro
 325 330 335
 Glu Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro
 340 345 350
 Asp Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys
 355 360 365
 Ile Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala
 370 375 380
 Glu Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
 385 390 395

<210> 931
 <211> 833
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(810)
 <223> FRXA02345

<400> 931
 ttt gct gcc att gaa tca gtc gaa gat gca gtg gga ttc ttc gaa gca 48
 Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu Ala
 1 5 10 15

Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
 260 265 270

taggtctttt ctgagcgcta gca

833

<210> 932

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 932

Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu Ala
 1 5 10 15

Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp Gly
 20 25 30

Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val
 35 40 45

Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val
 50 55 60

Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly
 65 70 75 80

Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val
 85 90 95

Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln
 100 105 110

Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val
 115 120 125

Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly
 130 135 140

Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr
 145 150 155 160

Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His
 165 170 175

Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala
 180 185 190

Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu
 195 200 205

Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp
 210 215 220

Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile
 225 230 235 240

Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu
 245 250 255

Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp

260

265

270

<210> 933

<211> 618

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(595)

<223> RXN02350

<400> 933

aagcatttct ccaacacttt tgatggacag attaacgctt aaaaggcctg ttatagactg 60

ataaacccgat acgtactttt cgcgcttaag gagaatttca gtg ggt cct cta gtt 115
 Val Gly Pro Leu Val
 1 5

ggt ttg atc atg ggt tcg gat tcg gat tgg gac act gta gcg cca gct 163
 Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala
 10 15 20

gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc 211
 Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val
 25 30 35

tct gca cac cgc acc cca gag aag atg ctc aac tac gca aag act gca 259
 Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn Tyr Ala Lys Thr Ala
 40 45 50

cat gag cgc ggc atc aag acg atc atc gcg tgt gct ggc ggc gct gca 307
 His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys Ala Gly Gly Ala Ala
 55 60 65

cac ctg cca ggc atg gtg gct gca gca act cca ctt cca gtc atc ggt 355
 His Leu Pro Gly Met Val Ala Ala Ala Thr Pro Leu Pro Val Ile Gly
 70 75 80 85

gtt cca cgc gca ttg aag gat ctc gac ggt ttg gat tcc ttg ctg tcc 403
 Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu Asp Ser Leu Leu Ser
 90 95 100

atc gtc cag atg cca ggc ggc gtt cca gtc gcc act gtc tcc atc ggt 451
 Ile Val Gln Met Pro Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly
 105 110 115

ggc gcg aag aat gca ggc cta ctt gcc gtt cgt att ctc ggt gct ggt 499
 Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly
 120 125 130

gat cct tct ttg gtc acg aag atg gcc gat tac caa gag aat atg gcg 547
 Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala
 135 140 145

aag gaa gtt gaa gcc aag gac gaa gca ctg aag aag cgc ttg ctc ggc 595
 Lys Glu Val Glu Ala Lys Asp Glu Ala Leu Lys Lys Arg Leu Leu Gly
 150 155 160 165

taatgaatcc gatcgtggtg ctg 618

<210> 934
 <211> 165
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 934
 Val Gly Pro Leu Val Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp
 1 5 10 15
 Thr Val Ala Pro Ala Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe
 20 25 30
 Glu Val Gly Val Val Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn
 35 40 45
 Tyr Ala Lys Thr Ala His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys
 50 55 60
 Ala Gly Gly Ala Ala His Leu Pro Gly Met Val Ala Ala Ala Thr Pro
 65 70 75 80
 Leu Pro Val Ile Gly Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu
 85 90 95
 Asp Ser Leu Leu Ser Ile Val Gln Met Pro Gly Gly Val Pro Val Ala
 100 105 110
 Thr Val Ser Ile Gly Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg
 115 120 125
 Ile Leu Gly Ala Gly Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr
 130 135 140
 Gln Glu Asn Met Ala Lys Glu Val Glu Ala Lys Asp Glu Ala Leu Lys
 145 150 155 160
 Lys Arg Leu Leu Gly
 165

~~<210> 935~~
 <211> 223
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(223)
 <223> FRXA02346

<400> 935
 aagcatttct ccaacacttt tgatggacag attaacgctt aaaaggcctg ttatagactg 60
 ataaaccgat acgtaacttt cgcgcttaag gagaatttca gtg ggt cct cta gtt 115
 Val Gly Pro Leu Val
 1 5
 ggt ttg atc atg ggt tcg gat tcg gat tgg gac act gta gcg cca gct 163
 Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala

```

                10                15                20
gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc 211
Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val
                25                30                35

tct gca cac cgc 223
Ser Ala His Arg
                40

<210> 936
<211> 41
<212> PRT
<213> Corynebacterium glutamicum

<400> 936
Val Gly Pro Leu Val Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp
  1                5                10                15

Thr Val Ala Pro Ala Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe
                20                25                30

Glu Val Gly Val Val Ser Ala His Arg
                35                40

<210> 937
<211> 252
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (20)..(229)
<223> FRXA02350

<400> 937
atactaggat ctcgacggtttg gat tcc ttg ctg tcc atc gtc cag atg cca 52
                Leu Asp Ser Leu Leu Ser Ile Val Gln Met Pro
                1                5                10

ggc ggc gtt cca gtc gcc act gtc tcc atc ggt ggc gcg aag aat gca 100
Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly Gly Ala Lys Asn Ala
                15                20                25

ggc cta ctt gcc gtt cgt att ctc ggt gct ggt gat cct tct ttg gtc 148
Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val
                30                35                40

acg aag atg gcc gat tac caa gag aat atg gcg aag gaa gtt gaa gcc 196
Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala
                45                50                55

aag gac gaa gca ctg aag aag cgc ttg ctc ggc taatgaatcc gatcgtggtg 249
Lys Asp Glu Ala Leu Lys Lys Arg Leu Leu Gly
                60                65                70

ctg 252

```

<210> 938
 <211> 70
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 938
 Leu Asp Ser Leu Leu Ser Ile Val Gln Met Pro Gly Gly Val Pro Val
 1 5 10 15
 Ala Thr Val Ser Ile Gly Gly Ala Lys Asn Ala Gly Leu Leu Ala Val
 20 25 30
 Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val Thr Lys Met Ala Asp
 35 40 45
 Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala Lys Asp Glu Ala Leu
 50 55 60
 Lys Lys Arg Leu Leu Gly
 65 70

<210> 939
 <211> 999
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(976)
 <223> RXA01087

<400> 939
 ggccttggca gagaactcgg ccccgaaggt cttgcttcct accaagaaac ccaaaccatt 60
 tatctctaata ccaaactgca cctatatata aggagtaaaa atg caa acc ctt gct 115
 Met Gln Thr Leu Ala
 1 5
 gct att gtt cgt gcc acg aag caa cct ttt gag atc acc acc att gat 163
 Ala Ile Val Arg Ala Thr Lys Gln Pro Phe Glu Ile Thr Thr Ile Asp
 10 15 20

ctg gat gca cca cga cca gat gaa gtt caa atc cgt gtt att gct gcc 211
 Leu Asp Ala Pro Arg Pro Asp Glu Val Gln Ile Arg Val Ile Ala Ala
 25 30 35
 gga gtg cgc cac act gac gca att gtt cgt gat cag att tac cca act 259
 Gly Val Arg His Thr Asp Ala Ile Val Arg Asp Gln Ile Tyr Pro Thr
 40 45 50
 ttt ctt ccc gca gtt ttc ggc cac gaa ggc gcc gga gta gtt gtc gcc 307
 Phe Leu Pro Ala Val Phe Gly His Glu Gly Ala Gly Val Val Val Ala
 55 60 65
 gtg ggt tct gca gtc acc tcg gtg aaa cca gat gac aag gta gtg ctg 355
 Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp Asp Lys Val Val Leu
 70 75 80 85
 gga ttc aac tct tgt ggc cag tgc ttg aag tgt ttg ggc ggt aag cct 403
 Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys Leu Gly Gly Lys Pro

90	95	100	
gcg tac tgt gag aaa ttc tat gac cgc aac ttc gca tgc acc cgc gat Ala Tyr Cys Glu Lys Phe Tyr Asp Arg Asn Phe Ala Cys Thr Arg Asp 105 110 115			451
gcc ggg cac act act ttg ttt acc cgt gca aca aaa gag cag gca gag Ala Gly His Thr Thr Leu Phe Thr Arg Ala Thr Lys Glu Gln Ala Glu 120 125 130			499
gcc atc atc gac acc ctt gat gat gtt ttc tac gat gcg gat gcg ggt Ala Ile Ile Asp Thr Leu Asp Asp Val Phe Tyr Asp Ala Asp Ala Gly 135 140 145			547
ttc ctg gca tac cca gca act ccc cca gag gct tcg gga gta agc gtg Phe Leu Ala Tyr Pro Ala Thr Pro Pro Glu Ala Ser Gly Val Ser Val 150 155 160 165			595
ttg gtt gtc gcg gct ggt acc tct gat ctc ccc caa gca aag gaa gca Leu Val Val Ala Ala Gly Thr Ser Asp Leu Pro Gln Ala Lys Glu Ala 170 175 180			643
cta cac act gcc tcc tac ttg ggg cgc tcc acc tca ctg att gtt gat Leu His Thr Ala Ser Tyr Leu Gly Arg Ser Thr Ser Leu Ile Val Asp 185 190 195			691
ttt gga gtg gct ggc atc cac cgc ctg ctt tca tac gaa gaa gaa ctc Phe Gly Val Ala Gly Ile His Arg Leu Leu Ser Tyr Glu Glu Glu Leu 200 205 210			739
cgc gct gcg ggc gtg ctc atc gtt gcc gct gga atg gat ggt gcg cta Arg Ala Ala Gly Val Leu Ile Val Ala Ala Gly Met Asp Gly Ala Leu 215 220 225			787
ccc gga gtt gtc gca ggc tta gtg tcc gca cct gtc gtc gca ctg cca Pro Gly Val Val Ala Gly Leu Val Ser Ala Pro Val Val Ala Leu Pro 230 235 240 245			835
acc tcc gtg gga tac ggc gca ggt gct gga gga atc gca cca ctt ctg Thr Ser Val Gly Tyr Gly Ala Gly Ala Gly Gly Ile Ala Pro Leu Leu 250 255 260			883
acc atg ctt aac gcc tgc gcg ccg gga gtt gga gtg gtc aac att gat Thr Met Leu Asn Ala Cys Ala Pro Gly Val Gly Val Val Asn Ile Asp 265 270 275			931
aac ggc tat gga gca gga cac ctg gct gcg cag att gcg gcg agg Asn Gly Tyr Gly Ala Gly His Leu Ala Ala Gln Ile Ala Ala Arg 280 285 290			976
taagggtttc gcaggagacg aac			999

<210> 940

<211> 292

<212> PRT

<213> Corynebacterium glutamicum

<400> 940

Met Gln Thr Leu Ala Ala Ile Val Arg Ala Thr Lys Gln Pro Phe Glu
1 5 10 15

Ile Thr Thr Ile Asp Leu Asp Ala Pro Arg Pro Asp Glu Val Gln Ile
 20 25 30
 Arg Val Ile Ala Ala Gly Val Arg His Thr Asp Ala Ile Val Arg Asp
 35 40 45
 Gln Ile Tyr Pro Thr Phe Leu Pro Ala Val Phe Gly His Glu Gly Ala
 50 55 60
 Gly Val Val Val Ala Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp
 65 70 75 80
 Asp Lys Val Val Leu Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys
 85 90 95
 Leu Gly Gly Lys Pro Ala Tyr Cys Glu Lys Phe Tyr Asp Arg Asn Phe
 100 105 110
 Ala Cys Thr Arg Asp Ala Gly His Thr Thr Leu Phe Thr Arg Ala Thr
 115 120 125
 Lys Glu Gln Ala Glu Ala Ile Ile Asp Thr Leu Asp Asp Val Phe Tyr
 130 135 140
 Asp Ala Asp Ala Gly Phe Leu Ala Tyr Pro Ala Thr Pro Pro Glu Ala
 145 150 155 160
 Ser Gly Val Ser Val Leu Val Val Ala Ala Gly Thr Ser Asp Leu Pro
 165 170 175
 Gln Ala Lys Glu Ala Leu His Thr Ala Ser Tyr Leu Gly Arg Ser Thr
 180 185 190
 Ser Leu Ile Val Asp Phe Gly Val Ala Gly Ile His Arg Leu Leu Ser
 195 200 205
 Tyr Glu Glu Glu Leu Arg Ala Ala Gly Val Leu Ile Val Ala Ala Gly
 210 215 220
 Met Asp Gly Ala Leu Pro Gly Val Val Ala Gly Leu Val Ser Ala Pro
 225 230 235 240
 Val Val Ala Leu Pro Thr Ser Val Gly Tyr Gly Ala Gly Ala Gly Gly
 245 250 255
 Ile Ala Pro Leu Leu Thr Met Leu Asn Ala Cys Ala Pro Gly Val Gly
 260 265 270
 Val Val Asn Ile Asp Asn Gly Tyr Gly Ala Gly His Leu Ala Ala Gln
 275 280 285
 Ile Ala Ala Arg
 290

<210> 941

<211> 1551

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1528)

<223> RXA00619

<400> 941

```

tcaaaggaag acaccattga aggtgtgcgc aaaatcggag aattcatcaa aaaatagcag 60

cgactagggtt agtttcgggtt cgtggggaat aataatttgc gtg gct gat aaa aag 115
                               Val Ala Asp Lys Lys
                               1           5

aag atc gca aac gtc ctg tcg aac cgt tac gcc tcc gcg gaa ctt tct 163
Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser
                10                15                20

aac ctg tgg agt gcc gaa gag aag atc atc atg gag cgc cag ctc tgg 211
Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp
                25                30                35

atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc 259
Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala
                40                45                50

gag gca att gaa tcc tat gaa gca gtg atc gac cag gtt gat ttg gca 307
Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala
                55                60                65

agc atc gcc gat cgt gag cgc gtc acc cgc cac gat gtg aag gcc cgc 355
Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg
                70                75                80                85

atc gaa gaa ttc aat gca ctg gct ggc cat gag cac atc cac aag ggc 403
Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly
                90                95                100

atg acc tcc cgc gac ctc acc gaa aat gtt gaa cag ctg cag atc cac 451
Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His
                105                110                115

cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct 499
Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala
                120                125                130

atc gga tcc cgc gca gcg cag tac caa agc ctg gtc atg gct ggc cgt 547
Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg
                135                140                145

tcc cac aac gtg gca gcg cag gca act acc ttg ggc aag cgt ttc gca 595
Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala
                150                155                160                165

acc gca gct gat gaa atg ctc gtg gca ctt gag cgc gtc acc gaa ctg 643
Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu
                170                175                180

ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc 691
Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly Pro Met Gly Thr Ala
                185                190                195

caa gac atg ctt gac ctc atg gaa ggc gac gag gct cgt ctc tcc gat 739

```

Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu Ala Arg Leu Ser Asp	
200 205 210	
ctg gaa acc cgc atc gca gca cac ctc ggc ttt gat cgc gtc ttc gac	787
Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe Asp Arg Val Phe Asp	
215 220 225	
tcc gtc ggc cag gtc tac cca cgt tcc ctt gac ttc gat gca gta tct	835
Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp Phe Asp Ala Val Ser	
230 235 240 245	
gct ctg gtt cag ctt ggc tcc ggc cca tca tcg ctg tcc cac acc att	883
Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser Leu Ser His Thr Ile	
250 255 260	
cgt ctc atg gcc ggc acc gaa act gtt acc gaa ggt ttt aag gaa ggc	931
Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu Gly Phe Lys Glu Gly	
265 270 275	
cag gtc ggt tcc tct gca atg cct cac aag atg aac gct cgc tcc tgt	979
Gln Val Gly Ser Ser Ala Met Pro His Lys Met Asn Ala Arg Ser Cys	
280 285 290	
gag cgc gtg ggc ggc ctg cag gtt att ctt cgc gga tac ctc acc atg	
1027	
Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg Gly Tyr Leu Thr Met	
295 300 305	
gtt gct gat ctt tcc ggc cag cag tgg aac gaa ggc gat gtc ttc tgc	
1075	
Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu Gly Asp Val Phe Cys	
310 315 320 325	
tcc gtg atc cgc cgc gtt gca ctg cca gac gca ttc ttc gcg att gac	
1123	
Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala Phe Phe Ala Ile Asp	
330 335 340	
gga atg ttt gaa act ttc ctg aca gtc ctg gat gaa ttc ggt gca ttc	
1171	
Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp Glu Phe Gly Ala Phe	
345 350 355	

cct gcc atg atc gag cgc gaa ctt gag cgt tac ctg cca ttc ctg gca	
1219	
Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr Leu Pro Phe Leu Ala	
360 365 370	
act acc cgt atc ctc atg gcc gct gtc cgc gca ggc gtt ggc cgc gaa	
1267	
Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala Gly Val Gly Arg Glu	
375 380 385	
acc gca cac gaa gta atc aag gaa aac gct gtc gcg gtt gcc ctc aac	
1315	
Thr Ala His Glu Val Ile Lys Glu Asn Ala Val Ala Val Ala Leu Asn	
390 395 400 405	
atg cgc gaa aat ggc ggt gac cag gac ctt atc cag cgc ctc gct gct	
1363	
Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile Gln Arg Leu Ala Ala	

410 415 420
 gat gag cgc ctc cca atg agc gaa gct gac ctt gag gca gcg ctg gct
 1411
 Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala
 425 430 435
 gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg
 1459
 Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val
 440 445 450
 ctc gac cgc att cag gtg ctt gtc gac gcc cac ccc ggc gcc gca gac
 1507
 Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp
 455 460 465
 tac cga cca ggt gag att ctt taaaggtttt taacggcgtt cac
 1551
 Tyr Arg Pro Gly Glu Ile Leu
 470 475
 <210> 942
 <211> 476
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 942
 Val Ala Asp Lys Lys Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala
 1 5 10 15
 Ser Ala Glu Leu Ser Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met
 20 25 30
 Glu Arg Gln Leu Trp Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly
 35 40 45
 Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp
 50 55 60
 Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His
 65 70 75 80
 Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu
 85 90 95
 His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu
 100 105 110
 Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile
 115 120 125
 Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu
 130 135 140
 Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu
 145 150 155 160
 Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu
 165 170 175

Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly
 180 185 190
 Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu
 195 200 205
 Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe
 210 215 220
 Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp
 225 230 235 240
 Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser
 245 250 255
 Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu
 260 265 270
 Gly Phe Lys Glu Gly Gln Val Gly Ser Ser Ala Met Pro His Lys Met
 275 280 285
 Asn Ala Arg Ser Cys Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg
 290 295 300
 Gly Tyr Leu Thr Met Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu
 305 310 315 320
 Gly Asp Val Phe Cys Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala
 325 330 335
 Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp
 340 345 350
 Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr
 355 360 365
 Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala
 370 375 380
 Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val
 385 390 395 400

Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile
 405 410 415
 Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu
 420 425 430
 Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser
 435 440 445
 Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His
 450 455 460
 Pro Gly Ala Ala Asp Tyr Arg Pro Gly Glu Ile Leu
 465 470 475

<210> 943
 <211> 1683

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1660)

<223> RXA02622

<400> 943

```

atcaagcagg ttgagcgtaa actcattgta gaagtcctga acagcgtgga attttcgcgt 60

caggggtggcg tacaactcaa ctggagaggc taaatccttc atg agc gat gat cgt 115
                                         Met Ser Asp Asp Arg
                                         1           5

aag gca att aaa cgc gca cta att agc gtg tat gac aag act ggc ctg 163
Lys Ala Ile Lys Arg Ala Leu Ile Ser Val Tyr Asp Lys Thr Gly Leu
                10                15                20

gag gat cta gcc cag gca ctt cac cgc gag aac gtg gaa att gtt tcc 211
Glu Asp Leu Ala Gln Ala Leu His Arg Glu Asn Val Glu Ile Val Ser
                25                30                35

acc gga tcc act gcg gcg aag att gct gag ctt ggt att cct gtt acc 259
Thr Gly Ser Thr Ala Ala Lys Ile Ala Glu Leu Gly Ile Pro Val Thr
                40                45                50

ccg gtt gag gag ctc acc ggt ttc cct gag tgc ctt gag ggc cgt gtg 307
Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys Leu Glu Gly Arg Val
                55                60                65

aag aca ctg cac cct aag gtt cac gct ggc atc ttg gcg gac acc cgc 355
Lys Thr Leu His Pro Lys Val His Ala Gly Ile Leu Ala Asp Thr Arg
                70                75                80                85

aag gaa gac cac ctg cgt cag ctc aag gaa ctt gag gtc gcc cca ttc 403
Lys Glu Asp His Leu Arg Gln Leu Lys Glu Leu Glu Val Ala Pro Phe
                90                95                100

cag ctt gtc gtg gtg aac ctg tac cca ttt gct gag acc gtt gcg tcc 451
Gln Leu Val Val Val Asn Leu Tyr Pro Phe Ala Glu Thr Val Ala Ser
                105                110                115

ggc gcc gat ttc gat gct tgc gtt gag cag atc gac atc gga ggc cca 499
Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile Asp Ile Gly Gly Pro
                120                125                130

tcc atg gtt cgt gct gcg gca aag aac cac cca tct gtc gct gtg gtt 547
Ser Met Val Arg Ala Ala Lys Asn His Pro Ser Val Ala Val Val
                135                140                145

gtt tca ccg aac cgc tac gag gat gtc cag gaa gct ttg aag acc ggt 595
Val Ser Pro Asn Arg Tyr Glu Asp Val Gln Glu Ala Leu Lys Thr Gly
                150                155                160                165

gga ttc tcc cgc gcg gag cgc acc aag ttg gct gct gag gct ttc cgc 643
Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala Ala Glu Ala Phe Arg
                170                175                180

cac acc gca acc tac gat gtc acc gtt gca acc tgg atg agc gag cag 691
His Thr Ala Thr Tyr Asp Val Thr Val Ala Thr Trp Met Ser Glu Gln

```

185	190	195	
ctg gct gcc gaa gat tct gag act gag ttc cca ggt tgg atc ggc acc			739
Leu Ala Ala Glu Asp Ser Glu Thr Glu Phe Pro Gly Trp Ile Gly Thr			
200	205	210	
acc aac acc ttg tcc cgc agc ttg cgt tac ggt gag aac cct cac cag			787
Thr Asn Thr Leu Ser Arg Ser Leu Arg Tyr Gly Glu Asn Pro His Gln			
215	220	225	
tct gca gct ttg tac gtg ggc aac acc cgc gga ctt gca cag gct aag			835
Ser Ala Ala Leu Tyr Val Gly Asn Thr Arg Gly Leu Ala Gln Ala Lys			
230	235	240	245
cag ttc cac ggc aag gaa atg agc tac aac aac tac acc gat tct gat			883
Gln Phe His Gly Lys Glu Met Ser Tyr Asn Asn Tyr Thr Asp Ser Asp			
250	255	260	
gct gca tgg cgt gca gcg tgg gat cac gag cgt cct tgt gta gct atc			931
Ala Ala Trp Arg Ala Ala Trp Asp His Glu Arg Pro Cys Val Ala Ile			
265	270	275	
atc aag cat gca aac cct tgt ggc att gct gtt tct gat gag tcc atc			979
Ile Lys His Ala Asn Pro Cys Gly Ile Ala Val Ser Asp Glu Ser Ile			
280	285	290	
gca gcg gca cac cgc gag gca cac gca tgt gac tct gtg tcc gca ttc			
1027			
Ala Ala Ala His Arg Glu Ala His Ala Cys Asp Ser Val Ser Ala Phe			
295	300	305	
ggt ggc gtc atc gcg tcc aac cgt gaa gtc agc gtt gag atg gct aac			
1075			
Gly Gly Val Ile Ala Ser Asn Arg Glu Val Ser Val Glu Met Ala Asn			
310	315	320	325
cag gtt gca gag atc ttc act gag gtc atc atc gct cct tcc tat gaa			
1123			
Gln Val Ala Glu Ile Phe Thr Glu Val Ile Ile Ala Pro Ser Tyr Glu			
330	335	340	
gag ggc gct gtg gag atc ctg agc cag aag aag aac atc cgt att ctt			
1171			
Glu Gly Ala Val Glu Ile Leu Ser Gln Lys Lys Asn Ile Arg Ile Leu			
345	350	355	
cag gct gaa gca cct gtg cgt aag ggc ttt gag tcc cgt gag atc tcc			
1219			
Gln Ala Glu Ala Pro Val Arg Lys Gly Phe Glu Ser Arg Glu Ile Ser			
360	365	370	
ggc ggt ctg ctt gtt cag gaa cgc gac ttg atc cac gct gag ggc gac			
1267			
Gly Gly Leu Leu Val Gln Glu Arg Asp Leu Ile His Ala Glu Gly Asp			
375	380	385	
aac tcc gca aac tgg act ctt gct gcc ggc tct gct gtt tct cct gag			
1315			
Asn Ser Ala Asn Trp Thr Leu Ala Ala Gly Ser Ala Val Ser Pro Glu			
390	395	400	405

gtt ctg aag gac ctg gag ttc gcg tgg act gca gtt cgt tcc gtg aag
1363

Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala Val Arg Ser Val Lys
410 415 420

tcc aac gca att ctg ttg gct aag aac ggc gct acc gtt ggc gtt ggc
1411

Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala Thr Val Gly Val Gly
425 430 435

atg gga cag gtc aac cgc gtt gac tct gct cgc ttg gct gtc gac cgt
1459

Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg Leu Ala Val Asp Arg
440 445 450

gca ggt gca gag cgc gct acc ggt tcc gtt gct gct tcc gat gcg ttc
1507

Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala Ala Ser Asp Ala Phe
455 460 465

ttc cca ttc gct gat ggc ttt gag gtt ctc gct gag gct ggc atc act
1555

Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala Glu Ala Gly Ile Thr
470 475 480 485

gct gtt gtg cag cct ggt gga tcc att cgc gac aac gag gtc att gag
1603

Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp Asn Glu Val Ile Glu
490 495 500

gca gcc aac aag gct ggc gtg acc atg tac ctg act ggt gcg cga cac
1651

Ala Ala Asn Lys Ala Gly Val Thr Met Tyr Leu Thr Gly Ala Arg His
505 510 515

ttc gct cac taaagttttt aaagatttcg ctt
1683

Phe Ala His
520

<210> 944

<211> 520

<212> PRT

<213> Corynebacterium glutamicum

<400> 944

Met Ser Asp Asp Arg Lys Ala Ile Lys Arg Ala Leu Ile Ser Val Tyr
1 5 10 15

Asp Lys Thr Gly Leu Glu Asp Leu Ala Gln Ala Leu His Arg Glu Asn
20 25 30

Val Glu Ile Val Ser Thr Gly Ser Thr Ala Ala Lys Ile Ala Glu Leu
35 40 45

Gly Ile Pro Val Thr Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys
50 55 60

Leu Glu Gly Arg Val Lys Thr Leu His Pro Lys Val His Ala Gly Ile
65 70 75 80

Leu Ala Asp Thr Arg Lys Glu Asp His Leu Arg Gln Leu Lys Glu Leu
 85 90 95
 Glu Val Ala Pro Phe Gln Leu Val Val Val Asn Leu Tyr Pro Phe Ala
 100 105 110
 Glu Thr Val Ala Ser Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile
 115 120 125
 Asp Ile Gly Gly Pro Ser Met Val Arg Ala Ala Ala Lys Asn His Pro
 130 135 140
 Ser Val Ala Val Val Val Ser Pro Asn Arg Tyr Glu Asp Val Gln Glu
 145 150 155 160
 Ala Leu Lys Thr Gly Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala
 165 170 175
 Ala Glu Ala Phe Arg His Thr Ala Thr Tyr Asp Val Thr Val Ala Thr
 180 185 190
 Trp Met Ser Glu Gln Leu Ala Ala Glu Asp Ser Glu Thr Glu Phe Pro
 195 200 205
 Gly Trp Ile Gly Thr Thr Asn Thr Leu Ser Arg Ser Leu Arg Tyr Gly
 210 215 220
 Glu Asn Pro His Gln Ser Ala Ala Leu Tyr Val Gly Asn Thr Arg Gly
 225 230 235 240
 Leu Ala Gln Ala Lys Gln Phe His Gly Lys Glu Met Ser Tyr Asn Asn
 245 250 255
 Tyr Thr Asp Ser Asp Ala Ala Trp Arg Ala Ala Trp Asp His Glu Arg
 260 265 270
 Pro Cys Val Ala Ile Ile Lys His Ala Asn Pro Cys Gly Ile Ala Val
 275 280 285
 Ser Asp Glu Ser Ile Ala Ala Ala His Arg Glu Ala His Ala Cys Asp
 290 295 300

Ser Val Ser Ala Phe Gly Gly Val Ile Ala Ser Asn Arg Glu Val Ser
 305 310 315 320
 Val Glu Met Ala Asn Gln Val Ala Glu Ile Phe Thr Glu Val Ile Ile
 325 330 335
 Ala Pro Ser Tyr Glu Glu Gly Ala Val Glu Ile Leu Ser Gln Lys Lys
 340 345 350
 Asn Ile Arg Ile Leu Gln Ala Glu Ala Pro Val Arg Lys Gly Phe Glu
 355 360 365
 Ser Arg Glu Ile Ser Gly Gly Leu Leu Val Gln Glu Arg Asp Leu Ile
 370 375 380
 His Ala Glu Gly Asp Asn Ser Ala Asn Trp Thr Leu Ala Ala Gly Ser
 385 390 395 400

Ala Val Ser Pro Glu Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala
405 410 415

Val Arg Ser Val Lys Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala
420 425 430

Thr Val Gly Val Gly Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg
435 440 445

Leu Ala Val Asp Arg Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala
450 455 460

Ala Ser Asp Ala Phe Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala
465 470 475 480

Glu Ala Gly Ile Thr Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp
485 490 495

Asn Glu Val Ile Glu Ala Ala Asn Lys Ala Gly Val Thr Met Tyr Leu
500 505 510

Thr Gly Ala Arg His Phe Ala His
515 520

<210> 945

<211> 1641

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1618)

<223> RXN00488

<400> 945

gtttgtggaat agcgtgtgag ctgcagcggg tatccgattt aaggacaagc tactaaagtt 60

tagataattg tggacacact atgaggagga actgtcgcac atg aca acc cag agc 115
Met Thr Thr Gln Ser
1 5

cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163
Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly
10 15 20

tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211
Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val
25 30 35

cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259
Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu
40 45 50

aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307
Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg
55 60 65

atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355
Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg
70 75 80 85

aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt	403
Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg	
90 95 100	
tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg	451
Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met	
105 110 115	
agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt	499
Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly	
120 125 130	
ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac	547
Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn	
135 140 145	
cgc gat atg cgt ttt gaa agc gac atg aac cgt cgt gtc gct gaa gtt	595
Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg Arg Val Ala Glu Val	
150 155 160 165	
atg acc cca atg cct ttg gtt gtt gct gaa gag ggc gtc acc aag gag	643
Met Thr Pro Met Pro Leu Val Val Ala Glu Glu Gly Val Thr Lys Glu	
170 175 180	
cag gct ctt gct ttg ctg tct gca aac aag gtg gag aag ctt cct atc	691
Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val Glu Lys Leu Pro Ile	
185 190 195	
atc gca aag gac ggc aag ctt gtc ggt ctg atc acg gtg aag gac ttc	739
Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile Thr Val Lys Asp Phe	
200 205 210	
gtt aag act gag cag cac ccg aac gca tcc aag gat gca tca ggt cgt	787
Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys Asp Ala Ser Gly Arg	
215 220 225	
ctg ctg gtt gcg gct ggc atc ggc acg ggc gag gag tca ttc cag cga	835
Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu Glu Ser Phe Gln Arg	
230 235 240 245	
gct ggt gcg ctt gcc gac gcc ggc gtc gac att ttg gtc gta gac tct	883
Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile Leu Val Val Asp Ser	
250 255 260	
gca cac gcc cat agc cgt gga gtt ttg gac atg gtg tcc cgc gtg aag	931
Ala His Ala His Ser Arg Gly Val Leu Asp Met Val Ser Arg Val Lys	
265 270 275	
aag tcg ttc ccc aag gtc gat atc gtt ggc ggc aac ttg gcg acc cgc	979
Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly Asn Leu Ala Thr Arg	
280 285 290	
gag gct gcg cag gcc atg att gaa gct ggc gca gac gct atc aag gtg	
1027	
Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala Asp Ala Ile Lys Val	
295 300 305	
ggg att ggc cca ggt tct att tgc acc act cgc gtt gtc gca ggt gtc	
1075	
Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg Val Val Ala Gly Val	

310 315 320 325
 ggt gca cct cag atc act gcg atc atg gag gca gct gtt cca gct cac
 1123
 Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His
 330 335 340
 aag gct ggc gtt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt
 1171
 Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly
 345 350 355
 gat atc gct aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc
 1219
 Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly
 360 365 370
 tcc atg ctg gct ggt acc gct gag gct cct ggt gag acc atc acc atc
 1267
 Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile
 375 380 385
 aac ggc aag cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct
 1315
 Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala
 390 395 400 405
 atg cag ggc cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac
 1363
 Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp
 410 415 420
 cgt tac ttc cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa
 1411
 Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu
 425 430 435
 ggc atc gaa ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att
 1459
 Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile
 440 445 450
 cac cag cag gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc
 1507
 His Gln Gln Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser
 455 460 465
 tcc acc att gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc
 1555
 Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser
 470 475 480 485
 gcg ggt ctg aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa
 1603
 Ala Gly Leu Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu
 490 495 500
 gct cct aac tac cac tagattttgc tcaacttaaagc agc
 1641
 Ala Pro Asn Tyr His
 505

<210> 946
 <211> 506
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 946

Met Thr Thr Gln Ser Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys
 1 5 10 15

Val Ala Leu Val Gly Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp
 20 25 30

Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr
 35 40 45

Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr
 50 55 60

Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile
 65 70 75 80

Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val
 85 90 95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr
 100 105 110

Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg
 115 120 125

Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val
 130 135 140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg
 145 150 155 160

Arg Val Ala Glu Val Met Thr Pro Met Pro Leu Val Val Ala Glu Glu
 165 170 175

Gly Val Thr Lys Glu Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val
 180 185 190

Glu Lys Leu Pro Ile Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile
 195 200 205

Thr Val Lys Asp Phe Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys
 210 215 220

Asp Ala Ser Gly Arg Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu
 225 230 235 240

Glu Ser Phe Gln Arg Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile
 245 250 255

Leu Val Val Asp Ser Ala His Ala His Ser Arg Gly Val Leu Asp Met
 260 265 270

Val Ser Arg Val Lys Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly
 275 280 285

Asn Leu Ala Thr Arg Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala
 290 295 300
 Asp Ala Ile Lys Val Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg
 305 310 315 320
 Val Val Ala Gly Val Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala
 325 330 335
 Ala Val Pro Ala His Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly
 340 345 350
 Met Gln Phe Ser Gly Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn
 355 360 365
 Ser Val Met Leu Gly Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly
 370 375 380
 Glu Thr Ile Thr Ile Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met
 385 390 395 400
 Gly Ser Met Gly Ala Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg
 405 410 415
 Ser Tyr Ser Lys Asp Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp
 420 425 430
 Lys Leu Val Pro Glu Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro
 435 440 445
 Ile Gly Asp Ile Ile His Gln Gln Val Gly Gly Leu Arg Ala Ala Met
 450 455 460
 Gly Tyr Thr Gly Ser Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe
 465 470 475 480
 Val Gln Ile Thr Ser Ala Gly Leu Lys Glu Ser His Pro His His Ile
 485 490 495
 Gln Gln Thr Val Glu Ala Pro Asn Tyr His
 500 505

 <210> 947
 <211> 574
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(574)
 <223> FRXA00492

 <400> 947
 gttgtggaat agcgtgtgag ctgcagcggg tatccgattt aaggacaagc tactaaagtt 60

 tagataattg tggacacact atgaggagga actgtcgcac atg aca acc cag agc 115
 Met Thr Thr Gln Ser
 1 5

cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163
 Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly
 10 15 20

tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211
 Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val
 25 30 35

cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259
 Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu
 40 45 50

aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307
 Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg
 55 60 65

atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355
 Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg
 70 75 80 85

aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt 403
 Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg
 90 95 100

tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg 451
 Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met
 105 110 115

agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt 499
 Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly
 120 125 130

ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac 547
 Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn
 135 140 145

cgc gat atg cgt ttt gaa agc gac atg 574
 Arg Asp Met Arg Phe Glu Ser Asp Met
 150 155

<210> 948

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 948

Met Thr Thr Gln Ser Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys
 1 5 10 15

Val Ala Leu Val Gly Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp
 20 25 30

Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr
 35 40 45

Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr
 50 55 60

Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile
 65 70 75 80

Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val
85 90 95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr
100 105 110

Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg
115 120 125

Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val
130 135 140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met
145 150 155

<210> 949

<211> 557

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(534)

<223> FRXA00488

<400> 949

cag atc act gcg atc atg gag gca gct gtt cca gct cac aag gct ggc 48
Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His Lys Ala Gly
1 5 10 15

ggt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt gat atc gct 96
Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala
20 25 30

aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc tcc atg ctg 144
Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu
35 40 45

gct ggt acc gct gag gct cct ggt gag acc atc acc atc aac ggc aag 192
Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys
50 55 60

cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct atg cag ggc 240
Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly
65 70 75 80

cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac cgt tac ttc 288
Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe
85 90 95

cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa ggc atc gaa 336
Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu
100 105 110

ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att cac cag cag 384
Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln
115 120 125

gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc tcc acc att 432

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile
 130 135 140

gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc gcg ggt ctg 480
 Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu
 145 150 155 160

aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa gct cct aac 528
 Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn
 165 170 175

tac cac tagattttgc tcacttaaag agc 557
 Tyr His

<210> 950

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 950

Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His Lys Ala Gly
 1 5 10 15

Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala
 20 25 30

Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu
 35 40 45

Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys
 50 55 60

Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly
 65 70 75 80

Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe
 85 90 95

Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu
 100 105 110

Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln
 115 120 125

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile
 130 135 140

Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu
 145 150 155 160

Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn
 165 170 175

Tyr His

<210> 951

<211> 1554

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1531)

<223> RXA02469

<400> 951

cgctcgaag cagtagtaaa gcagcaggaa ggtggtggaa agagcaattg aggtaccctt 60

gccgtgttca gggataactg attaatacaac taggagaccc atg cgt ttt ctt aac 115
 Met Arg Phe Leu Asn
 1 5

aat tcc aat ccg ccc tat gag ctg aca tat tcc gat gtg ttt atg gtg 163
 Asn Ser Asn Pro Pro Tyr Glu Leu Thr Tyr Ser Asp Val Phe Met Val
 10 15 20

cct tcg cgt tct gac gta ggc tcc cgc atg tcc gtg gat ctg cgc acc 211
 Pro Ser Arg Ser Asp Val Gly Ser Arg Met Ser Val Asp Leu Arg Thr
 25 30 35

aat gac gga act gga aca acc atc ccg ctc gtt gtg gca aac atg act 259
 Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val Val Ala Asn Met Thr
 40 45 50

gct gtt gct ggc cga cgc atg gct gag acc att gcg cgc cgc ggt ggc 307
 Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile Ala Arg Arg Gly Gly
 55 60 65

atg gcg att ctt ccg cag gat gtg ccc gcc gat att gct gca gag act 355
 Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp Ile Ala Ala Glu Thr
 70 75 80 85

atc gcg aat gtg aag aaa gcg gac ctg gtt ttt gat acc cca att acc 403
 Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe Asp Thr Pro Ile Thr
 90 95 100

gta aaa ccg cac cac acc gtg ggt tat gca cgc aac ttg atc cac aag 451
 Val Lys Pro His His Thr Val Gly Tyr Ala Arg Asn Leu Ile His Lys
 105 110 115

cgt gcg cac ggt gca gcc att gtt ttg gag ggc gat cag ccg gtc ggc 499
 Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly Asp Gln Pro Val Gly
 120 125 130

atc gtc acc gac aag gac ctc gaa ggc gca gac aac ttc act cag gtg 547
 Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp Asn Phe Thr Gln Val
 135 140 145

ggc acc ctc atg tcc acc tcc cta ttg acg ctg cct gag gat att tcc 595
 Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu Pro Glu Asp Ile Ser
 150 155 160 165

ccc gaa gac gcc ttc gga atc ctc cac gaa cac agc cgc aaa ctc gcc 643
 Pro Glu Asp Ala Phe Gly Ile Leu His Glu His Ser Arg Lys Leu Ala
 170 175 180

ccc gtc gtc gcg gct gac ggc tca ctc cgc ggc atc ctc acc cgc acc 691
 Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly Ile Leu Thr Arg Thr

185										190					195					
ggc gcc ctg cgc gcc acc atg tac aag ccg gct atc gac gcc aac ggc	739																			
Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala Ile Asp Ala Asn Gly																				
200 205 210																				
cgc ctg cga gtc ggc gcc gcc atc ggc atc aac ggc gac atc gaa gga	787																			
Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn Gly Asp Ile Glu Gly																				
215 220 225																				
cgc acc aaa acg ctt ctc gac gcc ggc gcc gac gtt cta gtc gtc gac	835																			
Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp Val Leu Val Val Asp																				
230 235 240 245																				
aca gca cac ggc cac caa tcc acc atg atc agc gcc ctc aaa cgc atc	883																			
Thr Ala His Gly His Gln Ser Thr Met Ile Ser Ala Leu Lys Arg Ile																				
250 255 260																				
cgc gca ctc gac gtc aac gtc ccc atc gtt gct ggc aac gtg gtc acc	931																			
Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala Gly Asn Val Val Thr																				
265 270 275																				
gcc gat ggt gtc cgc gac cta gtt gaa gca ggc gca aac atc atc aag	979																			
Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly Ala Asn Ile Ile Lys																				
280 285 290																				
gta ggc gtt gga cca ggc gca atg tgc acc acc cgc atg caa acc ggc																				
1027																				
Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr Arg Met Gln Thr Gly																				
295 300 305																				
gtt ggc cga cca cag ttc tcc gca gtg ctg gaa tgc gca gcc gaa gcc																				
1075																				
Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu Cys Ala Ala Glu Ala																				
310 315 320 325																				
cgc aaa ctc ggc gca cac gta tgg gca gac ggc gga gtc cgc gac ccc																				
1123																				
Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly Gly Val Arg Asp Pro																				
330 335 340																				
cgc gac gtc gcc ctg gca ctc gca gct ggc gcc tcc aac gtg atg gtc																				
1171																				
Arg Asp Val Ala Leu Ala Leu Ala Ala Gly Ala Ser Asn Val Met Val																				
345 350 355																				
gga tcc tgg ttc tcc gga acc tac gaa tcc ccc ggc gac ctc cgc ttc																				
1219																				
Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro Gly Asp Leu Arg Phe																				
360 365 370																				
gaa tcc gac gga cgc atg tac aaa gaa tcc ttc ggt atg gca tcc cgg																				
1267																				
Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe Gly Met Ala Ser Arg																				
375 380 385																				
cgc gcc gtg gaa agc cga aac caa aag gtc gaa gct ttc gaa aaa gca																				
1315																				
Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu Ala Phe Glu Lys Ala																				
390 395 400 405																				

cgc cgc gca atg ttc gaa gaa ggc atc tcc act gcc cgc atc tac att
1363

Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr Ala Arg Ile Tyr Ile
410 415 420

gac aaa cgc cac ggc gga gtc gag gac ctg gta gat caa atc atc tcc
1411

Asp Lys Arg His Gly Gly Val Glu Asp Leu Val Asp Gln Ile Ile Ser
425 430 435

ggt gtc cgc tcc tca ttc acc tac gca ggc gcc gat tcg att gaa acc
1459

Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala Asp Ser Ile Glu Thr
440 445 450

ttc ttc gaa cgc gcc acc gtc gga gtt caa tcc acc gaa ggc tac gca
1507

Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser Thr Glu Gly Tyr Ala
455 460 465

gaa gga aag cca cgc gct tcg cgt taagtgtgtg tgtgcctttg aga
1554

Glu Gly Lys Pro Arg Ala Ser Arg
470 475

<210> 952

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 952

Met Arg Phe Leu Asn Asn Ser Asn Pro Pro Tyr Glu Leu Thr Tyr Ser
1 5 10 15

Asp Val Phe Met Val Pro Ser Arg Ser Asp Val Gly Ser Arg Met Ser
20 25 30

Val Asp Leu Arg Thr Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val
35 40 45

Val Ala Asn Met Thr Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile
50 55 60

Ala Arg Arg Gly Gly Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp
65 70 75 80

Ile Ala Ala Glu Thr Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe
85 90 95

Asp Thr Pro Ile Thr Val Lys Pro His His Thr Val Gly Tyr Ala Arg
100 105 110

Asn Leu Ile His Lys Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly
115 120 125

Asp Gln Pro Val Gly Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp
130 135 140

Asn Phe Thr Gln Val Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu
145 150 155 160

Pro Glu Asp Ile Ser Pro Glu Asp Ala Phe Gly Ile Leu His Glu His
 165 170 175
 Ser Arg Lys Leu Ala Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly
 180 185 190
 Ile Leu Thr Arg Thr Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala
 195 200 205
 Ile Asp Ala Asn Gly Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn
 210 215 220
 Gly Asp Ile Glu Gly Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp
 225 230 235 240
 Val Leu Val Val Asp Thr Ala His Gly His Gln Ser Thr Met Ile Ser
 245 250 255
 Ala Leu Lys Arg Ile Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala
 260 265 270
 Gly Asn Val Val Thr Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly
 275 280 285
 Ala Asn Ile Ile Lys Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr
 290 295 300
 Arg Met Gln Thr Gly Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu
 305 310 315 320
 Cys Ala Ala Glu Ala Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly
 325 330 335
 Gly Val Arg Asp Pro Arg Asp Val Ala Leu Ala Leu Ala Gly Ala
 340 345 350
 Ser Asn Val Met Val Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro
 355 360 365
 Gly Asp Leu Arg Phe Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe
 370 375 380
 Gly Met Ala Ser Arg Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu
 385 390 395 400
 Ala Phe Glu Lys Ala Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr
 405 410 415
 Ala Arg Ile Tyr Ile Asp Lys Arg His Gly Gly Val Glu Asp Leu Val
 420 425 430
 Asp Gln Ile Ile Ser Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala
 435 440 445
 Asp Ser Ile Glu Thr Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser
 450 455 460
 Thr Glu Gly Tyr Ala Glu Gly Lys Pro Arg Ala Ser Arg
 465 470 475

<400> 953																	60
agggcgccag gggcatccag ccattaaagc ttttcgacga gccctcgccc atgtggccaa																	
agaatcttat ttggaggctc gtctagtaga gtgagttctt																	115
Val Ser Leu Gln Thr																	
1 5																	
aat cat cgc cca gta ctc gtc gtt gac ttc ggc gca cag tac gcg cag																	163
Asn His Arg Pro Val Leu Val Val Asp Phe Gly Ala Gln Tyr Ala Gln																	
10 15 20																	
ctg atc gca cgt cgt gtg cgt gag gcc ggc atc tac tcc gaa gtc atc																	211
Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile Tyr Ser Glu Val Ile																	
25 30 35																	
ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc																	259
Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala Lys Asn Ala Ala Ala																	
40 45 50																	
ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca																	307
Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr Ala Glu Gly Ala Pro																	
55 60 65																	
tcc ctt gac gct gag att ctt gat ctc gga ttg cca gta ttt ggc att																	355
Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu Pro Val Phe Gly Ile																	
70 75 80 85																	
tgc tac ggc ttc caa gcc atg acc cac gcg ctt ggt ggc acc gtt gcc																	403
Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu Gly Gly Thr Val Ala																	
90 95 100																	
aac acc ggt aag cgc gaa tac gga cgc acc gac atc aac gtt gcc ggt																	451
Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp Ile Asn Val Ala Gly																	
105 110 115																	
ggc gtc ctc cac gaa ggc ctc gaa gcc tgc cac aag gtg tgg atg agc																	499
Gly Val Leu His Glu Gly Leu Glu Ala Cys His Lys Val Trp Met Ser																	
120 125 130																	
cac ggc gac gcc gtc tct gaa gcc cca gaa ggt ttc gta gtc acc gcg																	547
His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly Phe Val Val Thr Ala																	
135 140 145																	
tcc tcc gaa ggt gcg cct gtc gca gct ttc gaa aac aag gaa cgc aaa																	595
Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu Asn Lys Glu Arg Lys																	
150 155 160 165																	
atg gct ggc gtg cag tac cac cca gag gta ttg cac tca cca cac ggc																	643
Met Ala Gly Val Gln Tyr His Pro Glu Val Leu His Ser Pro His Gly																	
170 175 180																	

cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag 691
 Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln
 185 190 195

aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc 739
 Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg
 200 205 210

gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt 787
 Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly
 215 220 225

gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac 835
 Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp
 230 235 240 245

cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag 883
 Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu
 250 255 260

cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg 931
 Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu
 265 270 275

gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt 979
 Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val
 280 285 290

acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc
 1027
 Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg
 295 300 305

tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt
 1075
 Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly
 310 315 320 325

tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg
 1123
 Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val
 330 335 340

gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac
 1171
 Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn
 345 350 355

gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg
 1219
 Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu
 360 365 370

cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc
 1267
 Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly
 375 380 385

ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt
 1315

Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu
 390 395 400 405

ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc
 1363

Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu
 410 415 420

cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt
 1411

Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu
 425 430 435

gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc
 1459

Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg
 440 445 450

tct gtt ggt gtt caa ggc gat ggc cgc acc tac gga cac cca atc gtc
 1507

Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr Gly His Pro Ile Val
 455 460 465

ctg cgc cca gtg tct tcc gaa gac gca atg acc gcc gac tgg acc cgc
 1555

Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr Ala Asp Trp Thr Arg
 470 475 480 485

ctg cca tac gag gtt ctg gag aag atc tcc acc cgc atc acc aac gaa
 1603

Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr Arg Ile Thr Asn Glu
 490 495 500

gtt cca gat gtg aac cgc gtg gtg ctg gac gta acc tcc aag cca cca
 1651

Val Pro Asp Val Asn Arg Val Val Leu Asp Val Thr Ser Lys Pro Pro
 505 510 515

gga acc atc gaa tgg gag taggccttaa atgagccttc gtt
 1692

Gly Thr Ile Glu Trp Glu
 520

<210> 954

<211> 523

<212> PRT

<213> Corynebacterium glutamicum

<400> 954

Val Ser Leu Gln Thr Asn His Arg Pro Val Leu Val Val Asp Phe Gly
 1 5 10 15

Ala Gln Tyr Ala Gln Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile
 20 25 30

Tyr Ser Glu Val Ile Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala
 35 40 45

Lys Asn Ala Ala Ala Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr
 50 55 60

Ala Glu Gly Ala Pro Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu
 65 70 75 80
 Pro Val Phe Gly Ile Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu
 85 90 95
 Gly Gly Thr Val Ala Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp
 100 105 110
 Ile Asn Val Ala Gly Gly Val Leu His Glu Gly Leu Glu Ala Cys His
 115 120 125
 Lys Val Trp Met Ser His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly
 130 135 140
 Phe Val Val Thr Ala Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu
 145 150 155 160
 Asn Lys Glu Arg Lys Met Ala Gly Val Gln Tyr His Pro Glu Val Leu
 165 170 175
 His Ser Pro His Gly Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile
 180 185 190
 Ala Gly Leu Glu Gln Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu
 195 200 205
 Ile Glu Lys Val Arg Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys
 210 215 220
 Gly Leu Ser Gly Gly Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln
 225 230 235 240
 Arg Ala Ile Gly Asp Arg Leu Thr Cys Val Phe Val Asp His Gly Leu
 245 250 255
 Leu Arg Ala Gly Glu Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala
 260 265 270
 Thr Gly Ala Lys Leu Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser
 275 280 285
 Lys Leu Ala Gly Val Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly
 290 295 300
 Ala Glu Phe Ile Arg Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu
 305 310 315 320
 Glu Ala Pro Glu Gly Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu
 325 330 335
 Tyr Pro Asp Val Val Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile
 340 345 350
 Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys
 355 360 365
 Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val
 370 375 380

Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe
385 390 395 400

Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp
405 410 415

Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu
420 425 430

Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu
435 440 445

Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr
450 455 460

Gly His Pro Ile Val Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr
465 470 475 480

Ala Asp Trp Thr Arg Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr
485 490 495

Arg Ile Thr Asn Glu Val Pro Asp Val Asn Arg Val Val Leu Asp Val
500 505 510

Thr Ser Lys Pro Pro Gly Thr Ile Glu Trp Glu
515 520

<210> 955

<211> 1486

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1486)

<223> FRXA00487

<400> 955

agggcgccag gggcatccag ccattaaagc ttttcgacga gccctcgccc atgtggccaa 60

agaatcttat ttggaggctc gtctagtaga gtgagttctt gtg agc ctt cag aca 115
Val Ser Leu Gln Thr
1 5

aat cat cgc cca gta ctc gtc gtt gac ttc ggc gca cag tac gcg cag 163
Asn His Arg Pro Val Leu Val Val Asp Phe Gly Ala Gln Tyr Ala Gln
10 15 20

ctg atc gca cgt cgt gtg cgt gag gcc ggc atc tac tcc gaa gtc atc 211
Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile Tyr Ser Glu Val Ile
25 30 35

ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc 259
Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala Lys Asn Ala Ala Ala
40 45 50

ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca 307
Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr Ala Glu Gly Ala Pro
55 60 65

tcc ctt gac gct gag att ctt gat ctc gga ttg cca gta ttt ggc att	355
Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu Pro Val Phe Gly Ile	
70 75 80 85	
tgc tac ggc ttc caa gcc atg acc cac gcg ctt ggt ggc acc gtt gcc	403
Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu Gly Gly Thr Val Ala	
90 95 100	
aac acc ggt aag cgc gaa tac gga cgc acc gac atc aac gtt gcc ggt	451
Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp Ile Asn Val Ala Gly	
105 110 115	
ggc gtc ctc cac gaa ggc ctc gaa gcc tgc cac aag gtg tgg atg agc	499
Gly Val Leu His Glu Gly Leu Glu Ala Cys His Lys Val Trp Met Ser	
120 125 130	
cac ggc gac gcc gtc tct gaa gcc cca gaa ggt ttc gta gtc acc gcg	547
His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly Phe Val Val Thr Ala	
135 140 145	
tcc tcc gaa ggt gcg cct gtc gca gct ttc gaa aac aag gaa cgc aaa	595
Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu Asn Lys Glu Arg Lys	
150 155 160 165	
atg gct ggc gtg cag tac cac cca gag gta ttg cac tca cca cac ggc	643
Met Ala Gly Val Gln Tyr His Pro Glu Val Leu His Ser Pro His Gly	
170 175 180	
cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag	691
Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln	
185 190 195	
aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc	739
Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg	
200 205 210	
gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt	787
Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly	
215 220 225	
gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac	835
Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp	
230 235 240 245	
cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag	883
Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu	
250 255 260	
cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg	931
Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu	
265 270 275	
gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt	979
Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val	
280 285 290	
acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc	1027
Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg	
295 300 305	

tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt
1075

Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly
310 315 320 325

tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg
1123

Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val
330 335 340

gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac
1171

Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn
345 350 355

gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg
1219

Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu
360 365 370

cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc
1267

Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly
375 380 385

ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt
1315

Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu
390 395 400 405

ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc
1363

Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu
410 415 420

cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt
1411

Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu
425 430 435

gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc
1459

Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg
440 445 450

tct gtt ggt gtt caa ggc gat ggc cgc
1486

Ser Val Gly Val Gln Gly Asp Gly Arg
455 460

<210> 956

<211> 462

<212> PRT

<213> Corynebacterium glutamicum

<400> 956

Val Ser Leu Gln Thr Asn His Arg Pro Val Leu Val Val Asp Phe Gly
1 5 10 15

Ala Gln Tyr Ala Gln Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile

20	25	30
Tyr Ser Glu Val Ile Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala		
35	40	45
Lys Asn Ala Ala Ala Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr		
50	55	60
Ala Glu Gly Ala Pro Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu		
65	70	75
Pro Val Phe Gly Ile Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu		
85	90	95
Gly Gly Thr Val Ala Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp		
100	105	110
Ile Asn Val Ala Gly Gly Val Leu His Glu Gly Leu Glu Ala Cys His		
115	120	125
Lys Val Trp Met Ser His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly		
130	135	140
Phe Val Val Thr Ala Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu		
145	150	155
Asn Lys Glu Arg Lys Met Ala Gly Val Gln Tyr His Pro Glu Val Leu		
165	170	175
His Ser Pro His Gly Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile		
180	185	190
Ala Gly Leu Glu Gln Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu		
195	200	205
Ile Glu Lys Val Arg Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys		
210	215	220
Gly Leu Ser Gly Gly Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln		
225	230	235
Arg Ala Ile Gly Asp Arg Leu Thr Cys Val Phe Val Asp His Gly Leu		
245	250	255
Leu Arg Ala Gly Glu Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala		
260	265	270
Thr Gly Ala Lys Leu Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser		
275	280	285
Lys Leu Ala Gly Val Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly		
290	295	300
Ala Glu Phe Ile Arg Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu		
305	310	315
Glu Ala Pro Glu Gly Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu		
325	330	335
Tyr Pro Asp Val Val Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile		
340	345	350

Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys
355 360 365

Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val
370 375 380

Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe
385 390 395 400

Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp
405 410 415

Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu
420 425 430

Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu
435 440 445

Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg
450 455 460

<210> 957

<211> 693

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(670)

<223> RXA02237

<400> 957

gacgagctgg gcattgctca gaccgctcgt cttcgtggac tgggtgaccg tcagcgtcgc 60

gcacttctcg agcgtttcgg cttcgaggat taattcttca gtg tcg ggc gat aac 115
Val Ser Gly Asp Asn
1 5

caa cta gga cgg ctc gta att ctt gcg ggc ccc tca gcg gtc ggt aaa 163
Gln Leu Gly Arg Leu Val Ile Leu Ala Gly Pro Ser Ala Val Gly Lys
10 15 20

tcg act gtg gtt gat cgc ctc cgc aat gac gtt cca aac ctg tat ttc 211
Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val Pro Asn Leu Tyr Phe
25 30 35

agt gtg tcg atg acc act agg gca cct cgt cct ggt gaa gtc gat gga 259
Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro Gly Glu Val Asp Gly
40 45 50

cgt gac tac ttc tat gtc act gca cag gaa ttt cag gac aaa atc gac 307
Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe Gln Asp Lys Ile Asp
55 60 65

tgt gga gag atg ctt gaa tgg gca gat atc cac ggc ggt ttg cag cgt 355
Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His Gly Gly Leu Gln Arg
70 75 80 85

tca ggc act cca gca ggt ccc gtc aat gag gct cgc caa aat ggt cgg 403

Ser Gly Thr Pro Ala Gly Pro Val Asn Glu Ala Arg Gln Asn Gly Arg
 90 95 100

cca gta ttg gtt gag gtt gat ctt gca gga gcc cga aac atc gct agc 451
 Pro Val Leu Val Glu Val Asp Leu Ala Gly Ala Arg Asn Ile Ala Ser
 105 110 115

tta att cca gat gca gaa acc atc ttc ctt gct cca cct tca tgg gaa 499
 Leu Ile Pro Asp Ala Glu Thr Ile Phe Leu Ala Pro Pro Ser Trp Glu
 120 125 130

gtt ttg gtt gaa cgc ctc act gga cgt ggc acc gaa agc gaa gac gtt 547
 Val Leu Val Glu Arg Leu Thr Gly Arg Gly Thr Glu Ser Glu Asp Val
 135 140 145

att gct cgc agg ctc gag acc gca cgc gaa gaa ttg gct gct cag agc 595
 Ile Ala Arg Arg Leu Glu Thr Ala Arg Glu Glu Leu Ala Ala Gln Ser
 150 155 160 165

gaa ttt aag cac gtc att atc aat gat gat gtg gat aca gcc gtc aag 643
 Glu Phe Lys His Val Ile Ile Asn Asp Asp Val Asp Thr Ala Val Lys
 170 175 180

gct att gag gat gtt ctc ctc ggc gct tagccaaaac atagagcggg 690
 Ala Ile Glu Asp Val Leu Leu Gly Ala
 185 190

agg 693

<210> 958

<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 958

Val Ser Gly Asp Asn Gln Leu Gly Arg Leu Val Ile Leu Ala Gly Pro
 1 5 10 15

Ser Ala Val Gly Lys Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val
 20 25 30

Pro Asn Leu Tyr Phe Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro
 35 40 45

Gly Glu Val Asp Gly Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe
 50 55 60

Gln Asp Lys Ile Asp Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His
 65 70 75 80

Gly Gly Leu Gln Arg Ser Gly Thr Pro Ala Gly Pro Val Asn Glu Ala
 85 90 95

Arg Gln Asn Gly Arg Pro Val Leu Val Glu Val Asp Leu Ala Gly Ala
 100 105 110

Arg Asn Ile Ala Ser Leu Ile Pro Asp Ala Glu Thr Ile Phe Leu Ala
 115 120 125

Pro Pro Ser Trp Glu Val Leu Val Glu Arg Leu Thr Gly Arg Gly Thr

```

130          135          140
Glu Ser Glu Asp Val Ile Ala Arg Arg Leu Glu Thr Ala Arg Glu Glu
145          150          155          160
Leu Ala Ala Gln Ser Glu Phe Lys His Val Ile Ile Asn Asp Asp Val
165          170          175
Asp Thr Ala Val Lys Ala Ile Glu Asp Val Leu Leu Gly Ala
180          185          190

<210> 959
<211> 1413
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1390)
<223> RXA01446

<400> 959
gatgattaaa aacctcacat gggatagtaa gatgaaataa cgtctgtgtg cgcacacgcg 60

tgcatactcc aacttcatgg atcggatgtg acgtaaacca atg gct gca atc gtt 115
Met Ala Ala Ile Val
1 5

att gtc ggc gct caa tgg ggc gat gaa ggc aaa ggt aag gcc acg gat 163
Ile Val Gly Ala Gln Trp Gly Asp Glu Gly Lys Gly Lys Ala Thr Asp
10 15 20

att ctc ggc gga ctc gtc gat tac gtg gtt aag ccc aat ggc ggt aac 211
Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys Pro Asn Gly Gly Asn
25 30 35

aac gct gga cac act gtt gtg gtc ggc ggc gag aag tac gag cta aag 259
Asn Ala Gly His Thr Val Val Val Gly Gly Glu Lys Tyr Glu Leu Lys
40 45 50

ctc ctt cct gcc ggc gtc ctc tcc gaa acg gcc acc cca att ttg ggc 307
Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala Thr Pro Ile Leu Gly
55 60 65

aac ggc gtt gtg atc aac ctt gag gca ctg ttc gaa gaa atc gac ggc 355
Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe Glu Glu Ile Asp Gly
70 75 80 85

ctt gag gct cgc ggt gcg gat gca tcc cgc ctg cgc atc tct gca aac 403
Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu Arg Ile Ser Ala Asn
90 95 100

gct cac ctg gtt gct cca tac cac cag gtg atg gac cgt gtt cag gaa 451
Ala His Leu Val Ala Pro Tyr His Gln Val Met Asp Arg Val Gln Glu
105 110 115

cgc ttc ctg ggc aag cgc gca atc ggc acc acc ggc cgt ggc atc ggc 499
Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr Gly Arg Gly Ile Gly
120 125 130

```

cca acc tac gcg gac aaa gta tcc cgc gtg gga atc cgt gtt caa gac 547
 Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly Ile Arg Val Gln Asp
 135 140 145

att ttc gac gaa tcc atc ctt cgt caa aaa gtc gaa tcc gcc ctg gat 595
 Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val Glu Ser Ala Leu Asp
 150 155 160 165

tac aaa aac cag gtg ctg gtg aag atg tac aac cgc aag gcc atc gtc 643
 Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn Arg Lys Ala Ile Val
 170 175 180

gct gag gaa atc gtg cag tac ttc ctc tcc tac gct gat cgt ctg cgc 691
 Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr Ala Asp Arg Leu Arg
 185 190 195

ccc atg gtc atc gat gcc acc ttg gtg ctc aac gag gca ctt gat cag 739
 Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn Glu Ala Leu Asp Gln
 200 205 210

ggc aag cac gtt ctt atg gaa ggt ggc cag gca acc atg ctc gac gtg 787
 Gly Lys His Val Leu Met Glu Gly Gly Gln Ala Thr Met Leu Asp Val
 215 220 225

gac cac ggc acc tac cca ttc gtc acc tcc tcc aac cca acc gcc ggt 835
 Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser Asn Pro Thr Ala Gly
 230 235 240 245

ggc gca agt gtt ggt tca ggt atc ggc cca acc aag atc acc agc tcc 883
 Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr Lys Ile Thr Ser Ser
 250 255 260

ttg ggt atc atc aag gcc tac acc act cgt gtt ggt gcc ggc cca ttc 931
 Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val Gly Ala Gly Pro Phe
 265 270 275

cca act gag ctg ttt gat aag tgg ggc gag tac ctg cag acc gtc ggt 979
 Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr Leu Gln Thr Val Gly
 280 285 290

ggc gag gtc ggc gtg aac acc ggc cgt aag cgt cgc tgt ggc tgg tac
 1027
 Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg Arg Cys Gly Trp Tyr
 295 300 305

gac tcc gtg att gct cgt tac gca tcc cgc gtc aac gga ttc acc gac
 1075
 Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val Asn Gly Phe Thr Asp
 310 315 320 325

tac ttc ctg acc aag cta gac gtg ctc acc ggc atc ggt gaa atc cca
 1123
 Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly Ile Gly Glu Ile Pro
 330 335 340

atc tgc gta gct tac gac gtt gat ggt gtt cgc cac gat gaa atg cca
 1171
 Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg His Asp Glu Met Pro
 345 350 355

ctg acc cag tca gag ttc cac cac gca acc cca atc ttt gaa acc atg
1219

Leu Thr Gln Ser Glu Phe His His Ala Thr Pro Ile Phe Glu Thr Met
360 365 370

cct gca tgg gac gaa gac atc acc gac tgc aag acc ttc gag gat ctt
1267

Pro Ala Trp Asp Glu Asp Ile Thr Asp Cys Lys Thr Phe Glu Asp Leu
375 380 385

cca caa aag gcc cag gac tac gtc cga cgt ctg gaa gaa ctc tct ggt
1315

Pro Gln Lys Ala Gln Asp Tyr Val Arg Arg Leu Glu Glu Leu Ser Gly
390 395 400 405

gct cgc ttc tcc tac atc ggt gtt gga cct ggt cgc gat cag acc atc
1363

Ala Arg Phe Ser Tyr Ile Gly Val Gly Pro Gly Arg Asp Gln Thr Ile
410 415 420

gtc ctg cat gac gta cta gct gac aac tagtactgat aaacatcagt
1410

Val Leu His Asp Val Leu Ala Asp Asn
425 430

gag
1413

<210> 960

<211> 430

<212> PRT

<213> Corynebacterium glutamicum

<400> 960

Met Ala Ala Ile Val Ile Val Gly Ala Gln Trp Gly Asp Glu Gly Lys
1 5 10 15

Gly Lys Ala Thr Asp Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys
20 25 30

Pro Asn Gly Gly Asn Asn Ala Gly His Thr Val Val Val Gly Gly Glu
35 40 45

Lys Tyr Glu Leu Lys Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala
50 55 60

Thr Pro Ile Leu Gly Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe
65 70 75 80

Glu Glu Ile Asp Gly Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu
85 90 95

Arg Ile Ser Ala Asn Ala His Leu Val Ala Pro Tyr His Gln Val Met
100 105 110

Asp Arg Val Gln Glu Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr
115 120 125

Gly Arg Gly Ile Gly Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly
130 135 140

Ile Arg Val Gln Asp Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val
 145 150 155 160
 Glu Ser Ala Leu Asp Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn
 165 170 175
 Arg Lys Ala Ile Val Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr
 180 185 190
 Ala Asp Arg Leu Arg Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn
 195 200 205
 Glu Ala Leu Asp Gln Gly Lys His Val Leu Met Glu Gly Gly Gln Ala
 210 215 220
 Thr Met Leu Asp Val Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser
 225 230 235 240
 Asn Pro Thr Ala Gly Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr
 245 250 255
 Lys Ile Thr Ser Ser Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val
 260 265 270
 Gly Ala Gly Pro Phe Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr
 275 280 285
 Leu Gln Thr Val Gly Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg
 290 295 300
 Arg Cys Gly Trp Tyr Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val
 305 310 315 320
 Asn Gly Phe Thr Asp Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly
 325 330 335
 Ile Gly Glu Ile Pro Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg
 340 345 350
 His Asp Glu Met Pro Leu Thr Gln Ser Glu Phe His His Ala Thr Pro
 355 360 365
 Ile Phe Glu Thr Met Pro Ala Trp Asp Glu Asp Ile Thr Asp Cys Lys
 370 375 380
 Thr Phe Glu Asp Leu Pro Gln Lys Ala Gln Asp Tyr Val Arg Arg Leu
 385 390 395 400
 Glu Glu Leu Ser Gly Ala Arg Phe Ser Tyr Ile Gly Val Gly Pro Gly
 405 410 415
 Arg Asp Gln Thr Ile Val Leu His Asp Val Leu Ala Asp Asn
 420 425 430

<210> 961

<211> 1551

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1528)

<223> RXA00619

<400> 961

tcaaaggaag acaccattga aggtgtgctgc aaaatcggag aattcatcaa aaaatagcag 60

cgactagggtt agtttcgggtt cgtggggaat aataatttgc gtg gct gat aaa aag 115
 Val Ala Asp Lys Lys
 1 5

aag atc gca aac gtc ctg tgc aac cgt tac gcc tcc gcg gaa ctt tct 163
 Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser
 10 15 20

aac ctg tgg agt gcc gaa gag aag atc atc atg gag cgc cag ctc tgg 211
 Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp
 25 30 35

atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc 259
 Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala
 40 45 50

gag gca att gaa tcc tat gaa gca gtg atc gac cag gtt gat ttg gca 307
 Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala
 55 60 65

agc atc gcc gat cgt gag cgc gtc acc cgc cac gat gtg aag gcc cgc 355
 Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg
 70 75 80 85

atc gaa gaa ttc aat gca ctg gct ggc cat gag cac atc cac aag ggc 403
 Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly
 90 95 100

atg acc tcc cgc gac ctc acc gaa aat gtt gaa cag ctg cag atc cac 451
 Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His
 105 110 115

cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct 499
 Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala
 120 125 130

atc gga tcc cgc gca gcg cag tac caa agc ctg gtc atg gct ggc cgt 547
 Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg
 135 140 145

tcc cac aac gtg gca gcg cag gca act acc ttg ggc aag cgt ttc gca 595
 Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala
 150 155 160 165

acc gca gct gat gaa atg ctc gtg gca ctt gag cgc gtc acc gaa ctg 643
 Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu
 170 175 180

ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc 691
 Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly Pro Met Gly Thr Ala
 185 190 195

caa gac atg ctt gac ctc atg gaa ggc gac gag gct cgt ctc tcc gat 739

Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu Ala Arg Leu Ser Asp	
200 205 210	
ctg gaa acc cgc atc gca gca cac ctc ggc ttt gat cgc gtc ttc gac	787
Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe Asp Arg Val Phe Asp	
215 220 225	
tcc gtc ggc cag gtc tac cca cgt tcc ctt gac ttc gat gca gta tct	835
Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp Phe Asp Ala Val Ser	
230 235 240 245	
gct ctg gtt cag ctt ggc tcc ggc cca tca tcg ctg tcc cac acc att	883
Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser Leu Ser His Thr Ile	
250 255 260	
cgt ctc atg gcc ggc acc gaa act gtt acc gaa ggt ttt aag gaa ggc	931
Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu Gly Phe Lys Glu Gly	
265 270 275	
cag gtc ggt tcc tct gca atg cct cac aag atg aac gct cgc tcc tgt	979
Gln Val Gly Ser Ser Ala Met Pro His Lys Met Asn Ala Arg Ser Cys	
280 285 290	
gag cgc gtg ggc ggc ctg cag gtt att ctt cgc gga tac ctc acc atg	
1027	
Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg Gly Tyr Leu Thr Met	
295 300 305	
gtt gct gat ctt tcc ggc cag cag tgg aac gaa ggc gat gtc ttc tgc	
1075	
Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu Gly Asp Val Phe Cys	
310 315 320 325	
tcc gtg atc cgc cgc gtt gca ctg cca gac gca ttc ttc gcg att gac	
1123	
Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala Phe Phe Ala Ile Asp	
330 335 340	
gga atg ttt gaa act ttc ctg aca gtc ctg gat gaa ttc ggt gca ttc	
1171	
Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp Glu Phe Gly Ala Phe	
345 350 355	

cct gcc atg atc gag cgc gaa ctt gag cgt tac ctg cca ttc ctg gca	
1219	
Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr Leu Pro Phe Leu Ala	
360 365 370	
act acc cgt atc ctc atg gcc gct gtc cgc gca ggc gtt ggc cgc gaa	
1267	
Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala Gly Val Gly Arg Glu	
375 380 385	
acc gca cac gaa gta atc aag gaa aac gct gtc gcg gtt gcc ctc aac	
1315	
Thr Ala His Glu Val Ile Lys Glu Asn Ala Val Ala Val Ala Leu Asn	
390 395 400 405	
atg cgc gaa aat ggc ggt gac cag gac ctt atc cag cgc ctc gct gct	
1363	
Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile Gln Arg Leu Ala Ala	

410 415 420
 gat gag cgc ctc cca atg agc gaa gct gac ctt gag gca gcg ctg gct
 1411
 Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala
 425 430 435
 gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg
 1459
 Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val
 440 445 450
 ctc gac cgc att cag gtg ctt gtc gac gcc cac ccc ggc gcc gca gac
 1507
 Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp
 455 460 465
 tac cga cca ggt gag att ctt taaaggtttt taacggcggtt cac
 1551
 Tyr Arg Pro Gly Glu Ile Leu
 470 475
 <210> 962
 <211> 476
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 962
 Val Ala Asp Lys Lys Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala
 1 5 10 15
 Ser Ala Glu Leu Ser Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met
 20 25 30
 Glu Arg Gln Leu Trp Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly
 35 40 45
 Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp
 50 55 60
 Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His
 65 70 75 80
 Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu
 85 90 95
 His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu
 100 105 110
 Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile
 115 120 125
 Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu
 130 135 140
 Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu
 145 150 155 160
 Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu
 165 170 175

Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly
 180 185 190
 Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu
 195 200 205
 Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe
 210 215 220
 Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp
 225 230 235 240
 Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser
 245 250 255
 Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu
 260 265 270
 Gly Phe Lys Glu Gly Gln Val Gly Ser Ser Ala Met Pro His Lys Met
 275 280 285
 Asn Ala Arg Ser Cys Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg
 290 295 300
 Gly Tyr Leu Thr Met Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu
 305 310 315 320
 Gly Asp Val Phe Cys Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala
 325 330 335
 Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp
 340 345 350
 Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr
 355 360 365
 Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala
 370 375 380
 Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val
 385 390 395 400
 Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile
 405 410 415
 Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu
 420 425 430
 Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser
 435 440 445
 Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His
 450 455 460
 Pro Gly Ala Ala Asp Tyr Arg Pro Gly Glu Ile Leu
 465 470 475

<210> 963

<211> 666

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(643)

<223> RXA00688

<400> 963

gcggaaccgc aatcttgatt cttgtatctg ttgcactgac cacagtgaag cagattgaga 60

```

gccagctcct gcaaagcaac tacgaaggac ttctaaaata atg cga ctc gta ctc 115
                                         Met Arg Leu Val Leu
                                           1           5

```

```

ctc gga cct ccc ggt gct ggt aag ggc acc cag gct gca att ctc tct 163
Leu Gly Pro Pro Gly Ala Gly Lys Gly Thr Gln Ala Ala Ile Leu Ser
                10                15                20

```

```

gag aag ctt ggc att cct cac att tct act ggc gat ctt ttc cgc gcc 211
Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly Asp Leu Phe Arg Ala
                25                30                35

```

```

aac att ggc gaa ggt acc cct ctg ggt atc gag gcc aag cag tac atc 259
Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu Ala Lys Gln Tyr Ile
                40                45                50

```

```

gac gct ggc aag ctg gtt cca acc gac gtg act gca cgt atg gtt gct 307
Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr Ala Arg Met Val Ala
                55                60                65

```

```

tcc cgc ctt gct gag tcc gat gct gca gaa ggc ttc ctt ttg gat ggt 355
Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly Phe Leu Leu Asp Gly
                70                75                80                85

```

```

ttc cca cgc acc gtt gag cag gct gac atc ttg gct aac ctg ctt tcc 403
Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu Ala Asn Leu Leu Ser
                90                95                100

```

```

gaa gct ggc cag acc ctc gat ggt gtt gtt aac tac cag gtt tct gaa 451
Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn Tyr Gln Val Ser Glu
                105                110                115

```

```

gac gtc gtc gtg gag cgc atg ctg tcc cgt ggt cgc gct gat gac aac 499
Asp Val Val Val Glu Arg Met Leu Ser Arg Gly Arg Ala Asp Asp Asn
                120                125                130

```

```

gaa gag acc atc cgc acc cgt ctc ggt gtc tac cgc gac gag act gct 547
Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr Arg Asp Glu Thr Ala
                135                140                145

```

```

cct ctg atc gat cac tac ggt gac aag atc atc aac att gag gct gaa 595
Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile Asn Ile Glu Ala Glu
                150                155                160                165

```

```

ggc gaa gtc gaa gag atc aac gct cgt acc ctc aag gca ctg ggc aaa 643
Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu Lys Ala Leu Gly Lys
                170                175                180

```

```

taagatttct tctctagtgc tgc 666

```

<210> 964
 <211> 181
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 964
 Met Arg Leu Val Leu Leu Gly Pro Pro Gly Ala Gly Lys Gly Thr Gln
 1 5 10 15
 Ala Ala Ile Leu Ser Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly
 20 25 30
 Asp Leu Phe Arg Ala Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu
 35 40 45
 Ala Lys Gln Tyr Ile Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr
 50 55 60
 Ala Arg Met Val Ala Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly
 65 70 75 80
 Phe Leu Leu Asp Gly Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu
 85 90 95
 Ala Asn Leu Leu Ser Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn
 100 105 110
 Tyr Gln Val Ser Glu Asp Val Val Val Glu Arg Met Leu Ser Arg Gly
 115 120 125
 Arg Ala Asp Asp Asn Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr
 130 135 140
 Arg Asp Glu Thr Ala Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile
 145 150 155 160
 Asn Ile Glu Ala Glu Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu
 165 170 175
 Lys Ala Leu Gly Lys
 180

<210> 965
 <211> 531
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(508)
 <223> RXA00266

<400> 965
 agtaggggat cgtccagcga agcgggtcgca gaggtgtgta ggaagctcta agtcgactta 60
 agtgcgcgaa gcagaccacc attaggtaga atcacccaac atg act gaa cgt act 115
 Met Thr Glu Arg Thr
 1 5

ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa 163
 Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu
 10 15 20

atc atc gca cgt att gag cgc aag ggc ctg aag ctc gct gct ctg gat 211
 Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys Leu Ala Ala Leu Asp
 25 30 35

ctg cgt gtt gca gac cgc gag acc gct gaa aag cac tac gaa gag cac 259
 Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys His Tyr Glu Glu His
 40 45 50

gct gac aag cca ttc ttc ggt gag ctc gtt gaa ttc atc acc tct gca 307
 Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu Phe Ile Thr Ser Ala
 55 60 65

cct ctg atc gca ggc atc gtc gaa ggc gag cgt gca atc gat gca tgg 355
 Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg Ala Ile Asp Ala Trp
 70 75 80 85

cgt cag ctt gct ggt ggc acc gac cca gtt gct aag gca acc cca ggc 403
 Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala Lys Ala Thr Pro Gly
 90 95 100

acc atc cgc ggc gat ttc gca ctg act gtt gga gag aac gtt gtt cac 451
 Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly Glu Asn Val Val His
 105 110 115

ggt tct gat tcc cca gag tcc gct gag cgc gag atc tcc atc tgg ttc 499
 Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu Ile Ser Ile Trp Phe
 120 125 130

cct aac ctg taatttttac ggtagaaaa aaa 531
 Pro Asn Leu
 135

<210> 966

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 966

Met Thr Glu Arg Thr Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn
 1 5 10 15

Gly His Val Gly Glu Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys
 20 25 30

Leu Ala Ala Leu Asp Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys
 35 40 45

His Tyr Glu Glu His Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu
 50 55 60

Phe Ile Thr Ser Ala Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg
 65 70 75 80

Ala Ile Asp Ala Trp Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala
 85 90 95

Lys Ala Thr Pro Gly Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly
 100 105 110

Glu Asn Val Val His Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu
 115 120 125

Ile Ser Ile Trp Phe Pro Asn Leu
 130 135

<210> 967

<211> 1245

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1222)

<223> RXA00489

<400> 967

cagcccgatt tcttcattga aatcgggctg tttctggttg tgctcgctat ctcgggtaaa 60

gtcttcgctg tatacgacca ttttaaggagg gcccgtcaca atg cgt gac cac gtt 115
 Met Arg Asp His Val
 1 5

gaa atc ggt atc ggc cgt gag gca cga cgc acc tac agc ttg gac gat 163
 Glu Ile Gly Ile Gly Arg Glu Ala Arg Arg Thr Tyr Ser Leu Asp Asp
 10 15 20

att tct gtc gtt tct agc cgc cgc acc cgt tca tcc aaa gat gtc gac 211
 Ile Ser Val Val Ser Ser Arg Arg Thr Arg Ser Ser Lys Asp Val Asp
 25 30 35

acc act tgg cat att gac gcc tac aag ttt gat ctg ccg ttc atg aat 259
 Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp Leu Pro Phe Met Asn
 40 45 50

cac cca agt gat gca ttg gca agc cct gag ttt gtc att gaa atg ggc 307
 His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe Val Ile Glu Met Gly
 55 60 65

aag cag ggt ggc ctt ggc gtg atc aac gct gag ggt ctg tgg ggt cgc 355
 Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu Gly Leu Trp Gly Arg
 70 75 80 85

cat gct gat ctc gat gag gcg atc gca aag gtg att gct gcg tat gag 403
 His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val Ile Ala Ala Tyr Glu
 90 95 100

gaa ggc gac cag gct gca gcc act cgc act ctt cag gag ctg cac gca 451
 Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu Gln Glu Leu His Ala
 105 110 115

gcg cca ctg gat act gag ctg ctg agt gag cgc att gcg cag gtt cgt 499
 Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg Ile Ala Gln Val Arg
 120 125 130

gat tcc ggt gag atc gtt gct gtg cgc gtg tct cca caa aat gtt cgt 547
 Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser Pro Gln Asn Val Arg

135	140	145	
gag atc gca cca atc gtc atc aag gca ggt gct gat ctg ctg gtt atc			595
Glu Ile Ala Pro Ile Val Ile Lys Ala Gly Ala Asp Leu Leu Val Ile			
150	155	160	165
cag ggc acc ctg atc tct gca gag cac gtc aac acc ggt gga gag gcc			643
Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn Thr Gly Gly Glu Ala			
170	175		180
ctg aac cta aag gaa ttc atc ggt tct ttg gat gtt cct gtc atc gct			691
Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp Val Pro Val Ile Ala			
185	190		195
ggt ggc gtg aac gat tac acc acc gcg ttg cac atg atg cgt acc ggt			739
Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His Met Met Arg Thr Gly			
200	205		210
gct gtg ggc atc atc gtc ggt ggc ggc gag aac acc aac agc cta gca			787
Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn Thr Asn Ser Leu Ala			
215	220		225
ttg ggc atg gag gta tcc atg gcc act gcg att gct gat gtc gct gcg			835
Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile Ala Asp Val Ala Ala			
230	235		245
gca cgt cgt gat tac ctg gat gag acc ggt gga cgt tac gtg cac atc			883
Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly Arg Tyr Val His Ile			
250	255		260
att gca gat gga agc att gaa aac tcc ggt gat gta gtc aag gct att			931
Ile Ala Asp Gly Ser Ile Glu Asn Ser Gly Asp Val Val Lys Ala Ile			
265	270		275
gcc tgt ggc gca gat gct gtg gtg ctg ggt tca ccg ttg gct cgc gct			979
Ala Cys Gly Ala Asp Ala Val Val Leu Gly Ser Pro Leu Ala Arg Ala			
280	285		290
gaa gaa gct gct gga aag ggc tac ttc tgg cca gca gtg gca gcg cac			
1027			
Glu Glu Ala Ala Gly Lys Gly Tyr Phe Trp Pro Ala Val Ala Ala His			
295	300		305
cct cgt ttc cca cgc ggt gtg gtt act gag tcc gtg gac ttg gat gag			
1075			
Pro Arg Phe Pro Arg Gly Val Val Thr Glu Ser Val Asp Leu Asp Glu			
310	315		320
gca gca cca agc ttg gag cag att ctg cat ggt ccg tct acg atg ccg			
1123			
Ala Ala Pro Ser Leu Glu Gln Ile Leu His Gly Pro Ser Thr Met Pro			
330	335		340
tgg ggt gtg gaa aac ttc gaa ggt gga tta aag cgt gcg ctg gct aag			
1171			
Trp Gly Val Glu Asn Phe Glu Gly Gly Leu Lys Arg Ala Leu Ala Lys			
345	350		355
tgt ggc tac acc gat ttg aag agc ttc caa aag gta agc ctg cac gtt			
1219			
Cys Gly Tyr Thr Asp Leu Lys Ser Phe Gln Lys Val Ser Leu His Val			

360

365

370

aac taggtgtgtg tactcgctc ttc
1245
Asn

<210> 968

<211> 374

<212> PRT

<213> Corynebacterium glutamicum

<400> 968

Met Arg Asp His Val Glu Ile Gly Ile Gly Arg Glu Ala Arg Arg Thr
1 5 10 15

Tyr Ser Leu Asp Asp Ile Ser Val Val Ser Ser Arg Arg Thr Arg Ser
20 25 30

Ser Lys Asp Val Asp Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp
35 40 45

Leu Pro Phe Met Asn His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe
50 55 60

Val Ile Glu Met Gly Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu
65 70 75 80

Gly Leu Trp Gly Arg His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val
85 90 95

Ile Ala Ala Tyr Glu Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu
100 105 110

Gln Glu Leu His Ala Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg
115 120 125

Ile Ala Gln Val Arg Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser
130 135 140

Pro Gln Asn Val Arg Glu Ile Ala Pro Ile Val Ile Lys Ala Gly Ala
145 150 155 160

Asp Leu Leu Val Ile Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn
165 170 175

Thr Gly Gly Glu Ala Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp
180 185 190

Val Pro Val Ile Ala Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His
195 200 205

Met Met Arg Thr Gly Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn
210 215 220

Thr Asn Ser Leu Ala Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile
225 230 235 240

Ala Asp Val Ala Ala Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly
245 250 255

70	75	80	85	
gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat				403
Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn				
	90	95	100	
tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg				451
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro				
	105	110	115	
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt				499
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly				
	120	125	130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac				547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp				
	135	140	145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg				595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro				
	150	155	160	165
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc				643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile				
	170	175	180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg				691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu				
	185	190	195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg				739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met				
	200	205	210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca				787
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro				
	215	220	225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa				835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu				
	230	235	240	245
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc ata				887
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile				
	250	255	260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca				931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro				
	265	270	275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa				979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu				
	280	285	290	
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc				1027
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg				
	295	300	305	
atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att				1075

Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile
 310 315 320 325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa
 1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu
 330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac
 1171

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp
 345 350 355

aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac
 1219

Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn
 360 365 370

tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc
 1267

Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser
 375 380 385

acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga
 1315

Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly
 390 395 400 405

tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg
 1363

Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu
 410 415 420

cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac
 1411

Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr
 425 430 435

ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa
 1459

Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu
 440 445 450

tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg
 1507

Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg
 455 460 465

acc ttg ggt gag gtg ccg ttt cgc taaagtctcg gaga
 1545

Thr Leu Gly Glu Val Pro Phe Arg
 470 475

<210> 970

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 970

Val Gln Lys Asp Ser Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp

1	5	10	15
Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala	20	25	30
Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val	35	40	45
Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg	50	55	60
Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr	65	70	75
Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu	85	90	95
Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp	100	105	110
Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu	115	120	125
Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu	130	135	140
Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn	145	150	155
Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile	165	170	175
Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val	180	185	190
Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe	195	200	205
Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val	210	215	220
Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr	225	230	235
Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro	245	250	255
Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn	260	265	270
Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala	275	280	285
Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met	290	295	300
Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln	305	310	315
Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile	325	330	335

Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu
 340 345 350

Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser
 355 360 365

Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn
 370 375 380

Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr
 385 390 395 400

Leu Ala Thr Asn Gly Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu
 405 410 415

Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln
 420 425 430

Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala
 435 440 445

Val Arg Ala Met Glu Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr
 450 455 460

Arg Lys Leu Arg Arg Thr Leu Gly Glu Val Pro Phe Arg
 465 470 475

<210> 971

<211> 1191

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1168)

<223> FRXA02281

<400> 971

aagatcaaca acgccgccga ggtcaacttg gaaattatca cgtgaggatt cttgcatacg 60

cctataaaag cacagttttg aatccacagg gcatcagggc gtg cag aaa gat agt 115
 Val Gln Lys Asp Ser
 1 5

gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu
 10 15 20

att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc gcc 307
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly
 55 60 65

tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc	355
Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg	
70 75 80 85	
gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat	403
Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn	
90 95 100	
tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg	451
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro	
105 110 115	
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt	499
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly	
120 125 130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac	547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp	
135 140 145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg	595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro	
150 155 160 165	
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc	643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile	
170 175 180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg	691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu	
185 190 195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg	739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met	
200 205 210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca	787
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro	
215 220 225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa	835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu	
230 235 240 245	
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc	883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile	
250 255 260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca	931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro	
265 270 275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa	979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu	
280 285 290	
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc	1027
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg	
295 300 305	

atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att
1075

Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile
310 315 320 325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa
1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu
330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc
1168

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser
345 350 355

tagtattcta tagtgcacc taa
1191

<210> 972

<211> 356

<212> PRT

<213> Corynebacterium glutamicum

<400> 972

Val Gln Lys Asp Ser Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp
1 5 10 15

Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala
20 25 30

Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val
35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile
165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val
180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe
195 200 205

Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val
210 215 220

Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr
225 230 235 240

Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro
245 250 255

Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn
260 265 270

Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala
275 280 285

Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met
290 295 300

Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln
305 310 315 320

Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile
325 330 335

Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu
340 345 350

Ile Tyr Gly Ser
355

<210> 973

<211> 1302

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) (1279)

<223> RXA00147

<400> 973

attgcatata atgcaatgaa ttgaataaac tacattcagg gttatcaacc agccaatttc 60

ttttaaaaag gcagacacac gaaaggcgac aacagtcacc gtg agt aaa gac acc 115
Val Ser Lys Asp Thr
1 5

acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg 163
Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu
10 15 20

gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc 211
Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile
25 30 35

ggc acc acc ctt ggt gag gca gtg ttc act acc gcc atg acc ggt tac 259

Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr Ala Met Thr Gly Tyr	
40 45 50	
caa gaa acc atg acc gat cct tcc tat cac cgc cag att gtt gtg gct	307
Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg Gln Ile Val Val Ala	
55 60 65	
acc gca cca cag atc ggc aac acc ggc tgg aac gat gag gac aac gag	355
Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn Asp Glu Asp Asn Glu	
70 75 80 85	
tcc cgc gac ggc aag att tgg gtt gca ggc ctt gtt atc cgc gac ctc	403
Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu Val Ile Arg Asp Leu	
90 95 100	
gca gca cgt gtg tcc aac tgg cgc gcc acc acc tcc ttg cag cag gaa	451
Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr Ser Leu Gln Gln Glu	
105 110 115	
atg gca ggc cag ggc atc gtc ggc atc ggc gga atc gac acc cgc gca	499
Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly Ile Asp Thr Arg Ala	
120 125 130	
ctg gtt cgc cac ctg cgc aat gaa ggt tcc att gca gcg ggc atc ttc	547
Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile Ala Ala Gly Ile Phe	
135 140 145	
tcc ggc gct gac gca cag cgc cca gtt gaa gaa ctc gta gag atc gtc	595
Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu Leu Val Glu Ile Val	
150 155 160 165	
aag aat cag cca gca atg acc ggc gca aac ctc tcc gtt gag gtc tct	643
Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu Ser Val Glu Val Ser	
170 175 180	
gct gat gaa acc tac gtc atc gaa gct gaa ggc gaa gag cgc cac acc	691
Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly Glu Glu Arg His Thr	
185 190 195	
gtc gtg gcc tac gac ctg ggc att aag caa aac acc cca cgt cgt ttc	739
Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn Thr Pro Arg Arg Phe	
200 205 210	
tct gca cgc ggt gtt cgc acc gtc atc gtg cct gct gaa acc cca ttc	787
Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro Ala Glu Thr Pro Phe	
215 220 225	
gag gat atc aag cag tac aac cca tca ggc gtg ttc atc tcc aac ggc	835
Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val Phe Ile Ser Asn Gly	
230 235 240 245	
cct ggc gat cct gca gca gca gac gtc atg gtt gat atc gtc cgc gaa	883
Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val Asp Ile Val Arg Glu	
250 255 260	
gtt ctt gaa gcc gac att cca ttc ttt ggc atc tgc ttc ggc aac cag	931
Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile Cys Phe Gly Asn Gln	
265 270 275	
att ctt ggc cgc gca ttc ggc atg gag acc tac aag ctg aag ttc ggc	979
Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe Gly	

280 285 290
 cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag atc
 1027
 His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile
 295 300 305
 gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca ggc
 1075
 Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly
 310 315 320 325
 cag gaa ttc gag acc gat ttc ggc act gca att gtc acc cac acc tgc
 1123
 Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys
 330 335 340
 ctc aac gac ggc gtc gtt gaa ggt att gcg ctg aag tcc gga cgc gca
 1171
 Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala
 345 350 355
 tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat gca
 1219
 Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala
 360 365 370
 agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag
 1267
 Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln
 375 380 385
 aag aaa ggc gca taaataacat gccaaagcgt tca
 1302
 Lys Lys Gly Ala
 390

<210> 974
 <211> 393
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 974
 Val Ser Lys Asp Thr Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser
 1 5 10 15
 Val Pro Ala Tyr Leu Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe
 20 25 30
 Gly Phe Gly Ala Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr
 35 40 45
 Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg
 50 55 60
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn
 65 70 75 80
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu
 85 90 95

Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr
 100 105 110
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly
 115 120 125
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile
 130 135 140
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu
 145 150 155 160
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu
 165 170 175
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly
 180 185 190
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn
 195 200 205
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro
 210 215 220
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val
 225 230 235 240
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val
 245 250 255
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile
 260 265 270
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr
 275 280 285
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His
 290 295 300
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu
 305 310 315 320
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile
 325 330 335
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu
 340 345 350
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala
 355 360 365
 Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met
 370 375 380
 Asp Ala Asp Ala Gln Lys Lys Gly Ala
 385 390

<210> 975

<211> 1059

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1036)

<223> RXA00145

<400> 975

ccccaccgca cgcgcggaag acgtttccgt catgcttaca gaaatcgacg gccgcgatgc 60

agtcacgctc acccgagaag actctgaagg ggattcctag atg aag cac ctc cta 115
 Met Lys His Leu Leu
 1 5

tcc att agc gat ctt tcc aaa gat gag att gtt gga ttg ctg gat gaa 163
 Ser Ile Ser Asp Leu Ser Lys Asp Glu Ile Val Gly Leu Leu Asp Glu
 10 15 20

gcg gat cgc ttt aag gag gtg ctc gaa gga cgt gaa gta aag aag ctg 211
 Ala Asp Arg Phe Lys Glu Val Leu Glu Gly Arg Glu Val Lys Lys Leu
 25 30 35

ccc acg ctg cgt ggt cgc acc att ttt acc ttg ttc tat gag aac tcc 259
 Pro Thr Leu Arg Gly Arg Thr Ile Phe Thr Leu Phe Tyr Glu Asn Ser
 40 45 50

acg cgc acc cgt tcg tcc ttt gaa acc gca gga aag tgg atg agc gcc 307
 Thr Arg Thr Arg Ser Ser Phe Glu Thr Ala Gly Lys Trp Met Ser Ala
 55 60 65

gat gtg att aac att tcg gcc tca tca tcc agc gtg aag aag ggc gag 355
 Asp Val Ile Asn Ile Ser Ala Ser Ser Ser Ser Val Lys Lys Gly Glu
 70 75 80 85

tcg ctg aaa gat acc ggc ttg act ttg tcg gca atc ggc gcg gat gcg 403
 Ser Leu Lys Asp Thr Gly Leu Thr Leu Ser Ala Ile Gly Ala Asp Ala
 90 95 100

atc atc atg cgc cac cca gcc tca ggc gcc gcg cag cag ctt gcg cag 451
 Ile Ile Met Arg His Pro Ala Ser Gly Ala Ala Gln Gln Leu Ala Gln
 105 110 115

ttc gtc gca cca ggt ggc aac ggc ccc agc gtg atc aac gcg ggt gac 499
 Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val Ile Asn Ala Gly Asp
 120 125 130

ggt tcg cac cag cac ccc acc cag gcg ctt ctc gac gct tta acc atc 547
 Gly Ser His Gln His Pro Thr Gln Ala Leu Leu Asp Ala Leu Thr Ile
 135 140 145

cgg cag cgc acc ggc cgc att gag gga ctc aaa gtt gtc atc gtg ggc 595
 Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys Val Val Ile Val Gly
 150 155 160 165

gac tgt ttg cac tcc cgg gtg gtg cgc tcc aat gtg gat ctg ctg tcc 643
 Asp Cys Leu His Ser Arg Val Val Arg Ser Asn Val Asp Leu Leu Ser
 170 175 180

act ttg ggc gca gag gta gtg ctg gtt gct cct ccg aca ctg ctt cct 691
 Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro Pro Thr Leu Leu Pro

185	190	195	
att ggt gtg gag aac tgg cca gtc cga ttc tcc tac gac atg gac gca			739
Ile Gly Val Glu Asn Trp Pro Val Arg Phe Ser Tyr Asp Met Asp Ala			
200	205	210	
gaa att gcc gac gcc gac gta gtg atg atg ctg cgc gtt cag caa gaa			787
Glu Ile Ala Asp Ala Asp Val Val Met Met Leu Arg Val Gln Gln Glu			
215	220	225	
cgc atg cag ggt ggt ttc ttc ccc tca cac cgt gag tac gca acg ctg			835
Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg Glu Tyr Ala Thr Leu			
230	235	240	245
tac ggc atg tcc aaa gag cgc gaa gct cgc ctc aag gac tcc gcc atc			883
Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu Lys Asp Ser Ala Ile			
250	255	260	
atc atg cac ccc gcc ccc atg ctt cgt gcc atg gaa att aac ttc cag			931
Ile Met His Pro Gly Pro Met Leu Arg Gly Met Glu Ile Asn Phe Gln			
265	270	275	
gtg gca gac gca cca cgc acc gcg gta ctg cag cag gta agc aac ggt			979
Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln Gln Val Ser Asn Gly			
280	285	290	
gtg cac atg cgc atg gcc att ttg ttc gcc ctg gtc gca ggc tct gac			
1027			
Val His Met Arg Met Ala Ile Leu Phe Ala Leu Val Ala Gly Ser Asp			
295	300	305	
gcg act atc taatcgcgac catctgatcg cga			
1059			
Ala Thr Ile			
310			
<210> 976			
<211> 312			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 976			
Met Lys His Leu Leu Ser Ile Ser Asp Leu Ser Lys Asp Glu Ile Val			
1	5	10	15
Gly Leu Leu Asp Glu Ala Asp Arg Phe Lys Glu Val Leu Glu Gly Arg			
20	25	30	
Glu Val Lys Lys Leu Pro Thr Leu Arg Gly Arg Thr Ile Phe Thr Leu			
35	40	45	
Phe Tyr Glu Asn Ser Thr Arg Thr Arg Ser Ser Phe Glu Thr Ala Gly			
50	55	60	
Lys Trp Met Ser Ala Asp Val Ile Asn Ile Ser Ala Ser Ser Ser Ser			
65	70	75	80
Val Lys Lys Gly Glu Ser Leu Lys Asp Thr Gly Leu Thr Leu Ser Ala			
85	90	95	

Ile Gly Ala Asp Ala Ile Ile Met Arg His Pro Ala Ser Gly Ala Ala
 100 105 110
 Gln Gln Leu Ala Gln Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val
 115 120 125
 Ile Asn Ala Gly Asp Gly Ser His Gln His Pro Thr Gln Ala Leu Leu
 130 135 140
 Asp Ala Leu Thr Ile Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys
 145 150 155 160
 Val Val Ile Val Gly Asp Cys Leu His Ser Arg Val Val Arg Ser Asn
 165 170 175
 Val Asp Leu Leu Ser Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro
 180 185 190
 Pro Thr Leu Leu Pro Ile Gly Val Glu Asn Trp Pro Val Arg Phe Ser
 195 200 205
 Tyr Asp Met Asp Ala Glu Ile Ala Asp Ala Asp Val Val Met Met Leu
 210 215 220
 Arg Val Gln Gln Glu Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg
 225 230 235 240
 Glu Tyr Ala Thr Leu Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu
 245 250 255
 Lys Asp Ser Ala Ile Ile Met His Pro Gly Pro Met Leu Arg Gly Met
 260 265 270
 Glu Ile Asn Phe Gln Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln
 275 280 285
 Gln Val Ser Asn Gly Val His Met Arg Met Ala Ile Leu Phe Ala Leu
 290 295 300
 Val Ala Gly Ser Asp Ala Thr Ile
 305 310

<210> 977
 <211> 1464
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1441)
 <223> RXA00146

<400> 977
 atggccattt tgttcgccct ggtcgcaggc tctgacgcga ctatctaatac gcgaccatct 60
 gatcgcgaaa ttctagaaaa ggtaacgagg gattaaagaa gtg gtt gac agc aac 115
 Val Val Asp Ser Asn
 1 5
 acc cag tat cca gaa acc ggc gca ctg gca ccg gct cct gca gac tca 163

Thr	Gln	Tyr	Pro	Glu	Thr	Gly	Ala	Leu	Ala	Pro	Ala	Pro	Ala	Asp	Ser		
				10					15					20			
ctc	cta	atc	agc	aac	gtt	ttg	gtc	tac	ggc	gaa	ggc	gag	cca	acg	aat	211	
Leu	Leu	Ile	Ser	Asn	Val	Leu	Val	Tyr	Gly	Glu	Gly	Glu	Pro	Thr	Asn		
			25					30					35				
gtg	ttt	gtt	aaa	gat	ggg	gtg	atc	gca	gct	atc	ggc	ggc	act	cat	gag	259	
Val	Phe	Val	Lys	Asp	Gly	Val	Ile	Ala	Ala	Ile	Gly	Gly	Thr	His	Glu		
		40					45					50					
gct	gac	cgc	acc	atc	gac	ggc	aat	ggg	gga	gtt	ctc	ctt	cca	ggg	ttc	307	
Ala	Asp	Arg	Thr	Ile	Asp	Gly	Asn	Gly	Gly	Val	Leu	Leu	Pro	Gly	Phe		
		55				60					65						
gtg	gac	atg	cac	gtt	cac	ctg	cgt	gag	cca	ggc	cgc	gaa	gac	act	gaa	355	
Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly	Arg	Glu	Asp	Thr	Glu		
	70				75					80					85		
acc	att	gcc	act	ggg	tct	gcc	gcc	gca	gcc	aag	ggc	gga	ttc	acc	gca	403	
Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys	Gly	Gly	Phe	Thr	Ala		
				90				95					100				
gta	ttc	acc	atg	gcg	aac	acc	act	cca	gtg	atg	gat	cag	ccg	gtt	atc	451	
Val	Phe	Thr	Met	Ala	Asn	Thr	Thr	Pro	Val	Met	Asp	Gln	Pro	Val	Ile		
			105					110					115				
gcg	gaa	tcc	gta	tgg	ttc	aag	ggc	caa	aac	att	ggc	ctg	tgc	gac	gtg	499	
Ala	Glu	Ser	Val	Trp	Phe	Lys	Gly	Gln	Asn	Ile	Gly	Leu	Cys	Asp	Val		
		120					125					130					
cat	cca	gtt	gga	tcc	atc	acc	aag	ggg	ctt	gag	ggc	aag	gag	ctt	act	547	
His	Pro	Val	Gly	Ser	Ile	Thr	Lys	Gly	Leu	Glu	Gly	Lys	Glu	Leu	Thr		
	135					140					145						
gag	ttc	ggc	atg	atg	gct	cgc	tct	gaa	gcc	aag	gtg	cgc	atg	ttc	tct	595	
Glu	Phe	Gly	Met	Met	Ala	Arg	Ser	Glu	Ala	Lys	Val	Arg	Met	Phe	Ser		
	150				155				160					165			
gat	gat	ggc	aag	tgc	gtc	gat	gat	cct	cag	gtc	atg	cgc	cgc	gcg	ctg	643	
Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val	Met	Arg	Arg	Ala	Leu		
			170					175						180			
gaa	tac	gcc	aag	ggc	atg	gac	gtt	ttg	atc	gcc	cag	cac	gct	gag	gat	691	
Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala	Gln	His	Ala	Glu	Asp		
		185					190					195					
cac	cgc	ctg	act	gag	ggc	gct	tca	gca	cac	gag	ggg	gaa	aac	gca	gct	739	
His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu	Gly	Glu	Asn	Ala	Ala		
		200				205						210					
cgt	ctg	ggg	ctg	cgc	ggc	tgg	cca	cgt	gtg	gct	gag	gaa	tcc	atc	gtg	787	
Arg	Leu	Gly	Leu	Arg	Gly	Trp	Pro	Arg	Val	Ala	Glu	Glu	Ser	Ile	Val		
	215					220					225						
gtg	cgc	gat	gcc	atc	atg	gct	cgt	gac	tac	ggc	aac	cgc	gtg	cac	atc	835	
Val	Arg	Asp	Ala	Ile	Met	Ala	Arg	Asp	Tyr	Gly	Asn	Arg	Val	His	Ile		
	230				235				240				245				
tgc	cac	gcc	tcc	act	gaa	ggc	acc	gtg	gag	ttg	ctt	cgt	tgg	gct	aag	883	
Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu	Leu	Arg	Trp	Ala	Lys		

250	255	260	
tcc cag ggc att cca atc acc gcg gaa gtc acc ccg cac cac ctc acc			931
Ser Gln Gly Ile Pro Ile Thr Ala Glu Val Thr Pro His His Leu Thr			
265	270	275	
ttg acc gat gag cgc ctg gaa acc tac gac gcg gtc aac aaa gtc aat			979
Leu Thr Asp Glu Arg Leu Glu Thr Tyr Asp Ala Val Asn Lys Val Asn			
280	285	290	
ccg cca ctg cgc gaa agc cgc gat gcc gaa gcg ctc aag aag gcg ctt			
1027			
Pro Pro Leu Arg Glu Ser Arg Asp Ala Glu Ala Leu Lys Lys Ala Leu			
295	300	305	
ctc gac ggc acc atc gat gtt gtt gca acc gac cac gct cct cac ggt			
1075			
Leu Asp Gly Thr Ile Asp Val Val Ala Thr Asp His Ala Pro His Gly			
310	315	320	325
tcc gaa gat aag tgc tgt gaa ttc gaa aac gcc aag cca ggc atg ctc			
1123			
Ser Glu Asp Lys Cys Cys Glu Phe Glu Asn Ala Lys Pro Gly Met Leu			
330	335	340	
gga ttg gaa acc tca ctg tcc atc atc gtg gac acc ttc gtt gcc acc			
1171			
Gly Leu Glu Thr Ser Leu Ser Ile Ile Val Asp Thr Phe Val Ala Thr			
345	350	355	
gga ctt gca gac tgg cgc ttt gtt gcg cgc gtg atg agt gaa cgc cca			
1219			
Gly Leu Ala Asp Trp Arg Phe Val Ala Arg Val Met Ser Glu Arg Pro			
360	365	370	
gca gaa atc acc cgt cta cca ggc cag ggt cgc cca atc gca gaa ggt			
1267			
Ala Glu Ile Thr Arg Leu Pro Gly Gln Gly Arg Pro Ile Ala Glu Gly			
375	380	385	
gag cca gca aac ctc gcg att gtt gat cca gga aaa acc tgg aca gca			
1315			
Glu Pro Ala Asn Leu Ala Ile Val Asp Pro Gly Lys Thr Trp Thr Ala			
390	395	400	405
tcc ggt gca gac ttt gcg tcc aag gct gaa aat acc cca ttt gag ggc			
1363			
Ser Gly Ala Asp Phe Ala Ser Lys Ala Glu Asn Thr Pro Phe Glu Gly			
410	415	420	
caa gaa ttc agt gcc aag gtc aca cac acc gtg ctt cgt ggc aag gtg			
1411			
Gln Glu Phe Ser Ala Lys Val Thr His Thr Val Leu Arg Gly Lys Val			
425	430	435	
act tgt gca gac gga gtt gca caa aac gct taacgggtgg gtgcatagta			
1461			
Thr Cys Ala Asp Gly Val Ala Gln Asn Ala			
440	445		

tgc
1464

<210> 978
<211> 447
<212> PRT
<213> Corynebacterium glutamicum

<400> 978

Val	Val	Asp	Ser	Asn	Thr	Gln	Tyr	Pro	Glu	Thr	Gly	Ala	Leu	Ala	Pro
1				5					10					15	
Ala	Pro	Ala	Asp	Ser	Leu	Leu	Ile	Ser	Asn	Val	Leu	Val	Tyr	Gly	Glu
			20					25					30		
Gly	Glu	Pro	Thr	Asn	Val	Phe	Val	Lys	Asp	Gly	Val	Ile	Ala	Ala	Ile
		35					40					45			
Gly	Gly	Thr	His	Glu	Ala	Asp	Arg	Thr	Ile	Asp	Gly	Asn	Gly	Gly	Val
	50					55				60					
Leu	Leu	Pro	Gly	Phe	Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly
65					70				75						80
Arg	Glu	Asp	Thr	Glu	Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys
				85					90						95
Gly	Gly	Phe	Thr	Ala	Val	Phe	Thr	Met	Ala	Asn	Thr	Thr	Pro	Val	Met
			100					105					110		
Asp	Gln	Pro	Val	Ile	Ala	Glu	Ser	Val	Trp	Phe	Lys	Gly	Gln	Asn	Ile
		115					120					125			
Gly	Leu	Cys	Asp	Val	His	Pro	Val	Gly	Ser	Ile	Thr	Lys	Gly	Leu	Glu
	130					135					140				
Gly	Lys	Glu	Leu	Thr	Glu	Phe	Gly	Met	Met	Ala	Arg	Ser	Glu	Ala	Lys
145					150					155					160
Val	Arg	Met	Phe	Ser	Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val
				165					170					175	
Met	Arg	Arg	Ala	Leu	Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala
			180					185					190		
Gln	His	Ala	Glu	Asp	His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu
	195						200					205			
Gly	Glu	Asn	Ala	Ala	Arg	Leu	Gly	Leu	Arg	Gly	Trp	Pro	Arg	Val	Ala
	210					215					220				
Glu	Glu	Ser	Ile	Val	Val	Arg	Asp	Ala	Ile	Met	Ala	Arg	Asp	Tyr	Gly
225					230					235					240
Asn	Arg	Val	His	Ile	Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu
				245					250					255	
Leu	Arg	Trp	Ala	Lys	Ser	Gln	Gly	Ile	Pro	Ile	Thr	Ala	Glu	Val	Thr
			260					265					270		